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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                        ö.
                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                     Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein search, using sw model
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1: /SIDS1/gcgdata/geneseq/geneseqp/AA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqp/AA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqp/AA1982.DAT:*

4: /SIDS1/gcgdata/geneseq/geneseqp/AA1983.DAT:*

5: /SIDS1/gcgdata/geneseq/geneseqp/AA1983.DAT:*

6: /SIDS1/gcgdata/geneseq/geneseqp/AA1985.DAT:*

7: /SIDS1/gcgdata/geneseq/geneseqp/AA1985.DAT:*

8: /SIDS1/gcgdata/geneseq/geneseqp/AA1987.DAT:*

9: /SIDS1/gcgdata/geneseq/geneseqp/AA1989.DAT:*

10: /SIDS1/gcgdata/geneseq/geneseqp/AA1990.DAT:*

11: /SIDS1/gcgdata/geneseq/geneseqp/AA1991.DAT:*

12: /SIDS1/gcgdata/geneseq/geneseqp/AA1993.DAT:*

13: /SIDS1/gcgdata/geneseq/geneseqp/AA1993.DAT:*

14: /SIDS1/gcgdata/geneseq/geneseqp/AA1993.DAT:*

15: /SIDS1/gcgdata/geneseq/geneseqp/AA1995.DAT:*

16: /SIDS1/gcgdata/geneseq/geneseqp/AA1995.DAT:*

17: /SIDS1/gcgdata/geneseq/geneseqp/AA1995.DAT:*

18: /SIDS1/gcgdata/geneseq/geneseqp/AA1997.DAT:*

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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /SIDS1/gcgdata/geneseq/geneseqp/AA1998.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp/AA1999.DAT:*
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R51003
W60037
W50287
R81882
W48976
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Compugen Ltd.
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                                                             Fusion protein TNF Sequence of a reco Antigenic peptide Human Fas antigen Plasmid pDC406/OX4 OX40/Fc mutein of Fusion protein of Integrin beta-1 ch Rabbit TGFbetaRII:
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acid	Completely humanis		d 1D10 a	Sequence of the li	Human kappa immuno	Human immunoglobul	n Interleuk	Ec soluble f	Human NR8alpha/IgG	ij.	Porcine CTLA-4-Ig	Human transmembran	oinding LFA-	3/IL-4 dual t	Aggrecanase artifi	ecanase artif	<pre>IgG1 polypeptide.</pre>	an interferc	IL4.Y124D/IgG1 pro	Anti-5T4 single ch	Heregulin-alpha fu	Human IL-6R-alpha-	Human interleukin-	SVPH1-26 disintegr	Human noggin/immun	[(453)IgG i	Human cytokine rec	acid sequ	an TGFbetaR1	NTNR alpha	rin ı	Bovine LOX-1 extra

ALIGNMENTS

RESULT
R24016
ID R2
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AC R2
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DT 26

R24016;

26-NOV-1992 (first entry)

R24016 standard; Protein; 485 AA.

PXXPX Lauffer L, EP488170-A. Region Key Tumour necrosis factor; TNF; IgG1; immunoglobulin G1 Fusion protein TNFRFc. 28-NOV-1990; 26-NOV-1991; 03-JUN-1992 Region Region Region Synthetic. (BEHW) BEHELNGWERKE AG. Oquendo P, Zettlmeissl G; 90DE-4037837. 91EP-0120187. /note= "human TNF extracellular receptor"
253..270
/note= "linker and hinge"
271..379
/note= "IgG1 CH2"
380..485
/note= "IgG1 CH3" Location/Qualifier

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Y54063 W71603

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell free receptor binding test contg. recombinant comprising carrier bound to fusion partner coupled and second, labelled binding partner, for receptor screening etc.
                                                                                                                                             Sequence
                                                                                                                                                                                                     07-OCT-1994
                                                                                                                                                                                                                                                          R51003;
                                                                                                                                                                                                                                                                                                               R51003 standard; Protein;
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                                                        Tumour necrosis factor receptor; chimeric antibody molecule
                                                                                                                TNFR/fc
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                                                                                                             of a recombinant human fusion protein.
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; Pred. No. 9.8e-87;
17; Mismatches 76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is contained in expression vector pCAV/NOT-TMFR (ATCC 68088). A
crecombinant chimeric antibody may be produced having TMFR sequences
csubstituted for the variable domains of either or both of the
immunoglobulin molecule heavy and light chains and having
unmodified constant region domains. A specific example of a TMFR/FC.
cfusion protein is given in 045252/FS1003. The rhu TMFR/FC fusion
cgene was created by ligating the following fragments into a cloning
vector: 1) an 867 bp Asp718-Pvu2 fragment from pCAV/NOT-TMFR (ATCC
cf0088) contg. the cDNA encoding the truncated TMFR. 2) a 700 bp
cstyl-Spel fragment from plasmid plxy498 coding for 232 AAs of the
cyector contg. the FC fragment of human IgG1. 3) An oligo linker, to
cfuse the truncated TMFR with the human IgG1 FC fragment. This
linker was created by PCR using primer 045225, which encodes the 3'
cend of the truncated TMF receptor and the 5' end of human IgG1,
and primer 045227, which is an antisense sequence encoding bps
cc 257-237 of human IgG1.
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q45224 is cDNA from clone 1 of library WI-26 VA4 of human fibroblast cell line WI-26 VA4. The mature full-length TNFRI is a glycoprotein having a mol. wt. of about 75-80 kDa.The cloning of the CDNA for TNFRI was described in Smith et al., Science 248:1019,1990. Clone 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treating TNF mediated inflammatory diseases with TNF antagonist esp. soluble form of TNF receptor, opt. as fusion protein with human immunoglobulin Fc region, esp. for treating arthritis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 32-34; 47pp; English.
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                                                     191 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
                                                                                                             248
                                                                                                                                                                                                                           123
                                                                                                                                                                                                                                                                132
 251 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
                                                                                                                                                                                   192 pcapgtfsnttsstdicrphqicnvvai----pgnasmdavctstsptrsmapgavhlpq
                                                                                                                                                                                                                                                                                                69 LQYVKQECNRTHNRVCECKEGRYLEI-----EFCLKHRSCPPGFGVVQAGTPERNTVCK 122
                                                                                                                                                                                                                                                                                                                                 74 yydq--taqmccskcspgqhakvfctktsdtvcdscedstytqlwnwvpeclscgsrcsc 131
                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 63.3
les 285; Conservative
                                                                                                                                                                                                                                                                                                                                                                        9 HYDEETSHOLLCDKCPPGTYLKOHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKE
                                                                                                                                                                                                                           RCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNS---
                                    gpsvflfppkpkdtlmisrtpevtcvvvdcshedpevkfnwycdgvevhnaktkpreegy
                                                                                                                                                                                                                                                            \tt dqvetqactreqnrictcrpgwycalskqegcrlcaplrkcrpgfgvarpgtets dvvck
                                                                                                         pvstrsqhtqptpepstapstsfllpmgpsppaegstgdepkscdkthtcppcpapellg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       518 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                        66.4%; Score 1488; 63.3%; Pred. No. 2. tive 21; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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2.2e-86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                      region. The invention provides the use of Fas antagonist as an agent for the treatment and prevention of apoptosis-related diseases. The Fas antagonist can be a partial Fas antigen peptide containing the extracellular part of the protein, but lacking the signal sequence, an anti-Fas antibody, or an anti-Fas ligand antibody, where the antibody is preferably a humanised antibody. The Fas antagonist is used in the treatment and prevention of diseases such as myocardial infarction, heart failure, ischemic heart disease, acute kidney failure, graft-versus-host disease, ischemic restenosis of the heart, liver or kidney, and endotoxic shock, and also as an organ preservative in transplantation. The agent is of low toxicity but effectively inhibits the Fas/Fas ligand
                                                                                                                                                                                                                                                                                                                                                                                                                         26-SEP-1997;
31-OCT-1996;
27-DEC-1996;
                                                                                                                                                                                                                                                    Use of Fas antagonist for treatment and prevention of apoptosis-related diseases - such as heart or kidney failure, graft-versus-host disease or liver disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fas ligand; Fas antagonist; apoptosis related disease; liver heart failure; kidney failure; graft-versus-host disease; an myocardial infarction; ischemic restenosis; endotoxic shock.
Sequence
                                                                                                                                                                                               This represents the antigenic peptide hFas (nd29) containing the Fc
                                                                                                                                                                                                                          Examples; Fig 5-9; 86pp; Japanese.
                                                                                                                                                                                                                                                                                                                          WPI; 1998-271925/24.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antigenic peptide hFas (nd29) containing Fc region
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 376 AA
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96JP-0290459.
96JP-0351718.
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30..376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                      Yatomi T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "hFas (nd29) protein'
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                                                                                                                                                                                                                                                                          Human; Fas antigen; derivative; apoptosis regulation; gene therapy; treatment; diabetes; arthritis; lupus; hepatitis; influenza; HIV; apoptosis modulation; immunoglobulin G1 Fc; IgG1 Fc; fusion.
          N-PSDB; V07004
                    WPI; 1997-558981/51
                                                                                                                                                                                                                                                      Homo sapiens.
                                        Nagata
                                                              (MOCH )
                                                                                                02-MAY-1996;
                                                                                                                    01-MAY-1997;
                                                                                                                                            13-NOV-1997
                                                                                                                                                                W09742319-A1
                                                                                                                                                                                                                                 Key
                                                                                                                                                                                                                                                                                                                       Human Fas antigen derivative/IgG1 Fc fusion
                                                                                                                                                                                                                                                                                                                                              16-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cdeghgleveinctrtqntkcrckpnffcnstvc---ehcdpctkcehgiikectltsnt 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CKELQYVKQE---CNRTHNRVCECKEGRYLEIEFCLKHRSCPP----GFGVVQAGTPERNT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lhhdgqfchk----pcppgerkardctvngdepdcvpcqegkeytdkahfsskcrrcr-l
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                                                                                                                                                                                                                                                                                                                                                                                         standard; Protein; 376
                                                              MOCHIDA PHARM CO LTD.
OSAKA BIOSCIENCE INST
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                                         Nakamura N;
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                                                                                              96JP-0135760
                                                                                                                    97WO-JP01502
                                                                                                                                                                                     /label= sig_peptide
17..376
/label= mat_peptide
                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60.4%;
67.3%;
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Pred. No. 5.5e-78
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Best Local Similarity
Matches 267; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fas antigen derivative containing modified extracellular region - has low antigenicity, promotes apoptosis and is useful in treatment of viral and other diseases  \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{
                                                          10-OCT-1995
                                                                                                                                         US5457035-A
                                                                                                                                                                                                                                                                                          OX40; OX40-L; cytokine; cell surface molecule; pDC406/OX40/Fc*; membrane glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                       Plasmid pDC406/OX40/Fc* encoding an OX40/Fc mutein protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAR-1996
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66.6%;
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Pred. No. 4.8e-77;
6; Mismatches 62;
                                                                                                                                                                                                                                                                                                                             plasmid;
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Best Local S
Matches 262
                   OX40/Fc; cytokine; T cell antigen; TH-2 immune response; OX40-L;
                                                                                                 OX40/Fc mutein
                                                                                                                                                                        25-SEP-1998 (first
                                                                                                                                                                                                                                                                                                                                 W48976 standard;
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and this was used, togethe screen various cell lines.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Column 35-38; 26pp; English.
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                                                                                                                             281 ALPAPIEKTISKAKGQPREPQYYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ
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les 262; Conser
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                                                                                                                                                                                                                                                                                                                                                                                SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
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                                                                                                                                                                                                                                             alpapiektiskakgqprepqvytlppsrdeltknqvsltclvkgfypsdiavewesngq
                                                                                                                                                                                                                                                                                                                                                 shedpevkfnwyvdgvevhnaktkpreegynstyrvvsvltvlhqdwlngkeykckvsnk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 crecqpghgmvnrcdhtrdtlchpcetgfyneavnydtckqctqcnh--rsgselkqnct
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  Protein; 438
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                                                                                                                                                                                                                                                                               The present sequence represents the OX40/Fc fusion protein that contains the extracellular domain of mouse OX40 fused to the mutated FC region of the human IgG1 antibody. The fusion protein was used for detecting cDNA clones encoding an OX40 ligand. The invention claims for a murine OX40-L cytokine (W48975) that binds to the murine T cell antigen, OX40. The OX40-L protein is claimed to be useful for co-stimulation of T-cell production and in binding assays for detecting OX40 or its homologues. The OX40-L protein is also claimed
                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                               Purified polypeptide OX-40 ligands - for co:stimulation production and binding assays for OX-40 and homologues
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22-JUN-1995;
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Chimeric -
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mes 262; Conserv
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DB; V32636.
                                                                                                                                                               CDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTD -- SWHTSDECLYCSPVCKELQYVKQECN 77
                                             ackpwtnctlsgkqtrhpasdsldavcedrsllatllwetqrptfrpttvqsttvwprts
                                                                      PCRKHTNCSVFGLLLTQKGNATHDNICSGNS------EST-----
                                                                                                                   RTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGFFSNETSSKA 137
                                                                                                                                          crecqpghgmvnrcdhtrdtlchpcetgfyneavnydtckqctqcnh--rsgselkqnct 96
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95US-0494574
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225
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                       -QKVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note- "Extracellular domain of mouse 207..438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "changed
mutant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                 59.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "changed mutant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gayle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Mutant Fc region of
                                                                                            -----pgtqprqdsgyklgvdcvpcppghfs--pgnnq
                                                                                                                                                                                        23;
                                                                                                                                                                                    Score 1332; DB 1y;
Pred. No. 1.2e-76;
""smatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from
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                                                                                                                                                                                                            Length
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                        The present sequence represents a fusion protien of the extracellular domain of a murine polypeptide, which a member of the cell development cycle protein family known as the Delta family of mammalian membrane surface-bound ligands, and the human immunoglobulin ([193]) FC portion. The murine delta-related protein gene is expressed within vascular endothelium indicates a role for the polypeptides in the control of endothelial cell biology. The murine polynucleotide was identified from a white adipose tissue cDNA library. The polypeptide is useful for identifying receptors, which bind to and/or are activated by the polypeptide. The polynucleotide is useful for identifying receptors, which bind to and/or are activated by the polypeptide. The polynucleotide is useful in gene therapy of cerebral autosomal dominant ateriopathy with subcortial infarcts and
                                                                                                                                                                                                                               Cell development cycle protein of delta family useful for various disorders associated with central nervous system e autosomal dominant ateriopathy and ischemic strokes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric
Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell development cycle; Delta family; membrane surface-bound ligand; endothelial cell biology; gene therapy; subcortial infarct; cerebral autosomal dominant ateriopathy; leucoencephalopathy; ischemic stroke; chimera.
                                                                                                                                                                                                                                                                                                                                 Shutter JR,
                                                                                                                                                                                                                                                                                                          WPI; 2000-195294/17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
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                                                                                                                                                                                                     Example 6; Page 169-171; 171pp; English.
                                                                                                                                                                                                                                                                                                                                                                 (AMGE-)
                                                                                                                                                                                                                                                                                                                                                                                              27-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200006726-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fusion protein of murine delta-related protein and human IgG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; Protein; 764 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "human IgG Fc portion"
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leucoencephalopathy, an autosomal

dominant disorder causing ischemic

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RESULT
W70540
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AC W7
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Best Local Similarity
Matches 270; Conserv
(TORA ) TORAY IND INC.
                                                                                                                                                                                                                                                                                                      W70540;
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                           29-AUG-1997;
29-JAN-1997;
                                                            29-JAN-1998;
                                                                                 30-JUL-1998.
                                                                                                      WO9832771-A1
                                                                                                                                                            Peptide
                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                       Integrin; beta-1 chain; immunoglobulin; chimeric; heterodimer complex;
inhibitor; binding; ligand; blood platelet; hemostatic; diagnostic age
                                                                                                                                                                                                                                                         Integrin beta-1 chain
                                                                                                                                                                                                                                                                                26-JAN-1999
                                                                                                                                                                                                                                                                                                                         W70540
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                                                                                                                                                                                                                                                                                                                                                                                         KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                  SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FGLLLTQKGNATHDNICS-----GN-----SESTQKVDKTHTCPPCPAPE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 r-spcahg-----gtchdlengpvc-tcpagfsgrrcevrithdacasgpcfngatc-- 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KHRSCPPGFGVVQAGT---PERNTVCKRCPDGF-----FSNETSSKAPCRKHTNCSV 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gsncekkvdrctsnpcangg-----qclnrgpsrtcrcrpgftgthcelhisdca 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TDSWH-----TSDECLYCSPVCKELQYVKQECNRTHNRVCECKEG-----RYLEIEFCL 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dqensyhcl---cppg-yygqhcehstlt-cadspcfnggscrernqgssyacecppnft 396
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                                                                                                                                                                                                                                                                                                                          standard;
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                           97JP-0234544.
97JP-0015118.
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                                                            98WO-JP00370
                                                                                                                                    /note= "signal peptide" 21..963
                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                          Protein;
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                                                                                                                          "mature protein"
                                                                                                                                                                                                                                                                                                                          963
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Pred. No. 3.
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PI Kainoh M, Tanaka T;

XX WPI; 1998-427881/36.

DR WPI; 1998-427881/36.

DR WPI; 1998-427881/36.

DR N-PSDB; v33773.

XX Integrin-immunoglobulin chimeric protein heterodimer complexes as PT platelet substitutes - contain the alpha and beta integrin chains PT platelet substitutes - contain the alpha and beta integrin chains PT platelet substitutes - contain the alpha and beta integrin chains PT presence of plasma components

XX Integrin-immunoglobulin chimeric protein heterodimer complexes that CC comprise an integrin alpha or beta chain associated with an immunoglobulin light or heavy chain. These chimeric proteins form CC immunoglobulin chain and an immunoglobulin chain; the protein beta chain and an immunoglobulin chain; CC the immunoglobulin chain in the ach case may be a heavy chain, or one of the CC many be a light chain. The integrin alpha chain is preferably alpha 4 crainpha 2 and the integrin beta chain is preferably beta 1. Animal cells transformed with vectors containing the DNA coding for the above chimeric CC proteins can be used in the preparation of the chimeric proteins and CC their heterodimer complexes. The heterodimer complexes, which are useful CC integrins to their ligands, function as blood platelet substitutes and CC integrins to their ligands, function as blood platelet substitutes and SQ Sequence 963 AA;
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멍 δÃ 밁 δÃ 밁 δÃ 밁 Qy 밁 Ş 밁 δÃ В δÃ 밁 δÃ 밁 Best Local Similarity Matches 272; Conserv Query Match 352 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 400 674 561 441 17:2 501 794 77 34 TAKWKTVCAPCPDHY----YTDSWHTSDECLYCSPVCKELQYVKQ KAKGQPREPQYTTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS NTVCKRCPDGFFSNETSSKAP------CRKH----ldsdgsfflyskltvdksrwqqgnvfscsvmhealhnhytqkslslspg yvdgvevhnaktkpreegynstyrvvsvltvlhqdwlngkeykckvsnkalpapiektis esrdklpqpvqpdpvshckekdvddcwfyftysvngnnevmvhvvenpecptgpedpeep --vck-ctdpkfqgqtcemcqtclgvcaehkecvqcrafnkgekkdtctqecsyfnitkv drsnglicggngvckcrvcecnpnytgsacdcsldtstceasngqicngrgicecg----ETFPPKYLHYDEETS--HQLLCD-----KCPPGT-----YLKQHC NRTHN------GFGVVQAGTPER 117 $\verb|ecstdevnsedmday| crkensseics | nn geover growth remains | growth remains | for the continuous continuous | for the continuous | for$ dsfkirplgfteevevilgyicececqsegipespkchegngtfecgacrcnegrvgrhc kakgqprepqvytlppsrdeltkpqvsltclvkgfypsdiavewesngqpennykttppv Conservative 56.1%; 31; Score 1256; DB 19; Pred. No. 1.7e-71; 1; Mismatches 90; -----TNCSVFGLLLT Length Indels 136; -----EC 962 EST Gaps 673 351 291 231 733 616 560 76 500 33 793 14;

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W73513
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                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 257; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transforming growth factor-beta receptor treat fibroproliferative disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fusion protein; fib
glomerulonephritis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAR-1999
                                                                                                                                                                                                                                                                                                                                             angioplasty, to prevent restenosis or scarring and reclosing of arteries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   collagen vascular disorder; therapy; rabbit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rabbit TGFbetaRII:Fc protein
                                     136
119 pkcimkek--kvfgetffmcscstdecndhiifseeyttsspdlvdkthtcppcpapell 176
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                                                                                                      RVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRCPD-----GFFSNETSS 135
                                 KAPCRKHTNCSVFG---LLLTQKGNATHDNICSGNSESTQK---VDKTHTCPPCPAPELL 189
                                                                                                                                          wtriastipphvqksvnndmmvtdnnyavkfpqlckfcdvrsstcdnqkscmsncsit-- 74:
                                                                                                                                                                              WKTVCAPCPDHYY----TDSWHTSDE------CLYC---SPYCKELQYVKQECNRTHN 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gotwals P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 18-19; 70pp;
                                                                                                                                                                                                                                                                                                           388
                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                  55.9%; Score 1252.5; D 65.7%; Pred. No. 1e-71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Koteliansky V,
                                                                                                                                                                                                                 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
                                                                                                                                                                                                                 Mismatches
                                                                   -avwrkndenitletvchdpklayhgflledsas
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Y54063
      The present sequence represents a splice variant of a rabbit transforming growth factor-beta (TGF-beta) type II receptor fused to the Fc portion of human IgG1. The fusion protein has higher affinity for TGF-beta than fusion proteins comprising the non-variant form of the receptor. The fusion protein contains soluble TGF-beta receptor constructs that are devoid of a transmembrane region (and are secreted from the cell) but retain the ability to bind TGF-beta. The protein competitively inhibits binding of TGF-beta to cellular receptors and/or forms an inactive complex with TGF-beta. The protein is used to reduce levels of TGF-beta, for treatment of arthritic conditions associated with overexpression of TGF-beta, especially fibroproliferative diseases, e.g. renal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Splice variant; rabbit; transforming growth factor-beta; TGF-beta; type II receptor; Fc portion; human IgG1; fusion protein; arthritis; fibroproliferative disease; renal; intra-ocular; pulmonary; fibrosis; diabetic nephropathy; glomerulonephritis; collagen vascular disease; proliferative vitreoretinopathy; myelofibrosis; systemic sclerosis;
                                                                                                                                                                                                          Disclosure; Page 62-63; 69pp; English.
                                                                                                                                                                                                                                             New fusion protein of a splice variant of transforming growth factor-beta receptor, for inhibiting the growth factor, e.g. in treatment of fibrosis
                                                                                                                                                                                                                                                                                                          WPI; 2000-106083/09.
N-PSDB; Z45251, Z452
                                                                                                                                                                                                                                            treatment of fibrosis
                                                                                                                                                                                                                                                                                                                                                        Koteliansky V, Gotwals
                                                                                                                                                                                                                                                                                                                                                                                                                         16-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9965948-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of TGF-beta type II receptor variant/IgG1 fusion
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                                                                                                                                                                                                                                                                                                                                                                                          (BIOJ ) BIOGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            post-radiation fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polymyositis; scleroderma; dermatomyositis; systemic lupus erythematosus;
restenosis; wound; connective tissue production; adhesion; scarring;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGFSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
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                                               24-OCT-1997;
18-FEB-1997;
                                                                                      17-FEB-1998;
                                                                                                                                       WO9836072-A1
                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                Human;
                                                                                                                                                                                                                                                       Human neurturin receptor alpha/Fc sequence (IfF2a) fusion protein.
                                                                                                                                                                                                                                                                                 19-NOV-1998
                                                                                                                                                                                                                                                                                                          W71603
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                                                                                                               20-AUG-1998.
                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                 neurturin receptor alpha; NTNR-alpha; variant; chimeric; protein; immunoadhesion; ret-expressing cell; neurologic
                                                                                                                                                                                                    haematological disease
           GENENTECH
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Pred. No. 1e-71;
7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Page 81-83; 116pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polypeptide(s) based on human
related nucleic acid - useful for
ret-expressing cells for treating
haematological diseases
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                                                                                                                               346 KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 HCTAKWKTVCAPCP-DHY--------YTDSWHTSDECLYCSPVCKELQYV
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                                                                                                   evkfnwyvdgvevhnaktkpreegynstyrvvsvltvlhqdwlngkeykckvsnkalpap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55.8%; Score 1249.
63.6%; Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DВ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71;
                                                                                                                                  400
                                                                                                       663
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                                                                                                                                                                                                                                                                                                                         431
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Y80123

Y80123 standard;

Protein;

19-MAY-2000

(first entry)

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Best-Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a neurturin receptor alpha (NTNR alpha). NTNR alpha binds neurturin. The NTNR alpha nucleic acid molecule is useful for the expression of NTNR alpha, which may be used to identify agonist and antagonist compounds having therapeutic applications, such
                                                                                                                                                                                                                                                                                                                                                                                                                                                    as enhancing splenic haematopoiesis, treating anaemia, thrombocytopaenia, hypoplasia, or haemorrhage. The present sequence is a NTNR alpha and IgG (immunoglobulin G) fusion protein from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleic acid molecule encodes a neurturin receptor-alpha amino acid sequence excluding the N-terminal signal peptide \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                          present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-181808/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hynes MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-FEB-1997;
09-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC.
                  346
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                                                                                                                                                                                                379
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                                                                                                                                                                                                                                                                                               274 ncrasyqtvts-cpadnyqaclgsyagmigfdmtpnyvdssptg---ivvspwc----
                                                                                                                                                                                                                                                                        73
                                                                                                                                                                                                                                                                                                                         32 HCTAKWKTVCAPCP-DHY------YIDSWHTSDECLYCSPVCKELQYV 72
                                                                                                                                                                                                                                                                                                                                                                ocal Similarity
  KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                        gprd---pvdkthtcppcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedp
                                        IEKTISKAKGQPREPQVYTLPPSRDELIKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY
                                                                                                                                                                     GNSESTQKVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 225
                                                                                                                                                                                                                    ERNTYCKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHD------NICS 165
                                                                                                                                                                                                                                               --scrgsgnmeeece--kflr-dftenpclrnaiqafgngtdvnvspkgpsfqatqaprv 378
                                                                                                                                                                                                                                                                       KQECNRTHNRVCECKEGRYLEIEF----CLKH------RSCP--PGFGVVQAGTP 115
                                                                                                                                                                                             ekt---pslpddlsdstslgtsvittctsvqeqgl----kannskelsmcftelttniip 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NTNR alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neurturin receptor alpha; NTNR alpha; splenic haematopoiesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Column 91-96; 78pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     thrombocytopaenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosenthal A,
                                                                                                                                                                                                                                                                                                                                                                                                                   664 AA;
                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0038839
97US-0049818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and IgG fusion
                                                                                                                                                                                                                                                                                                                                                               55.8%;
                                                                                                                                                                                                                                                                                                                                                    23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypoplasia; haemorrhage
                                                                                                                                                                                                                                                                                                                                                               Score 1249.5; D
Pred. No. 3e-71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₽
G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            占
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Best Local
                                                                                                                                                           Matches
                                                                                                                                                                                                                                      extracellular domain of a mammalian oxidized LDL (low density lipoprotein) receptor, fused to a partial heavy chain of a mammalian immunoglobulin containing all or part of the constant region. Oxidized LDL is a denatured form of LDL occurring in patients having arteriosclerosis or hyperlipidaemia, and the fusion peptide can be used for the assay of oxidized LDL in biological samples from such patients, for the diagnosis of the disorders. It can also be used therapeutically for the prevention and treatment of arteriosclerosis and hyperlipidaemia. The present sequence represents a chimeric protein immunoglobulin IgGl Fc region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-DEC-1998;
19-DEC-1997;
09-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 12; Page 75-79; 105pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric -
                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fusion peptide for assay of oxidized LDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-418906/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kakutani M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NISB ) JAPAN TOBACCO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bovine LOX-1 extracellular region/human IgG1 Fc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y24153 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fusion protein;
                                                    135
  188
                                                                             102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     609 kttppvldsdgsfflyskltvdksrwqqgnvfscsvmhealhnhytqkslslspg 663
                        144 --- NCSVFGLLLTQKGNATHDNICSGNSESTQKVDKTHTCPPCPAPELLGGPSVFLFPPK 200
                                                                                                       79
                                                                                                                               43 PCPDHYYTDSWHTSDECLYCSPVCKELQYVKQECNRTHNRVCECKEGRYLE-IEFCLKHR 101
sfp:/wmglsmrkpnyswlwedgtpltphlfriqgavsrmypsg-----tcayiqrgtv
                                                                             SCPPGFGVV-----QAGTP-----ERNTVCKRCPDGFFSNETSSKAPCRKHT- 143
                                                                                                     pcpqdwl---wh-eencyqfssgsfnweksqenclsldahllkinstdelefiqqmiahs 134
                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo
                                                                                                                                                                                                                           445 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos sp
                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Masaki T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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97JP-0364981.
98JP-0349648.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oxidised; arteriosclerosis; hyperlipidaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chimeric protein.
                                                                                                                                                                      55.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor; detection;
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                                                                                                                                                           23;
                                                                                                                                                        Score 1249; DB 20;
Pred. No. 2e-71;
3; Mismatches 67;
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                                                                                                                                                           Indels
                                                                                                                                                                                    Length
                                                                                                                                                         36;
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for treating of particularly n
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18-FEB-1997;
09-JUN-1997;
       The present sequence represents rat neurturin receptor alpha (NTNR-alpha)/Fc sequence (IFF2a) fusion protein, from an example of the present invention. NTNR-alpha proteins can be used: (a) to identify molecules that bind specifically to it (potential agonists and antagonists) and to purify such compounds; (b) to modulate response of cells to neurturin (NTN); (c) to increase survival of Ret-expressing cells or to activate Ret on the surface of cells (soluble glial derived neurotrophic factor receptor (GDNFR alpha) may be used the same way); (d) to increase the half-life of cognate ligands (especially NTN); (e) diagnostically to determine serum levels of its ligands; and (f) as animal feed additive or molecular weight marker. NTNR-alpha, its genes, (ant)agonists and antisense nucleic acids, are useful in vivo or ex vivo for treating conditions related to abnormal NTN activity or response, particularly neurological (central or enteric), renal or haematopoietic
                                                                                                                                                                                                                                                              New polypeptide(s) based on human neurturin receptor alpha and related nucleic acid - useful for increasing survival of ret-expressing cells for treating e.g. neurological, renal and haematological diseases
                                                                                                                                                                                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-467175/40
                                                                                                                                                                                                                                    Example 3; Page 84-86; 116pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neurturin receptor alpha; NTNR-alpha; variant; chimeric; protein; immunoadhesion; ret-expressing cell; neurologic; haematological disease.
                                                                                                                                                                                                                                                                                                                                                                                   Klein RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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97US-0802805.
97US-0871913.
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                                                                                                                                                                                                                                                                                                                                                                                   Rosenthal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alpha/Fc sequence (IfF2a) fusion
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Matches 261;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (spleen) diseases or injuries. Ab may be agonists or antagonists for therapeutic use (e.g. as antagonists to treat excessive/unwanted NTNR-alpha expression, e.g. in some tumours), also reagents for immunoassay and affinity purification.
          N-PSDB; Z91460
                     WPI; 2000-181808/16
                                        Hynes MA, Rosenthal
                                                                                  18-FEB-1997;
09-JUN-1997;
                                                                                                                                                             US6025157-A
                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                anaemia; thrombocytopaenia; hypoplasia;
                                                                                                                                                                                                                                                Rat NTNR alpha and
                                                                                                                                                                                                                                                                                                                Y80124 standard;
                                                                                                                   24-OCT-1997;
                                                                                                                                                                                                                            Human; neurturin receptor alpha; NTNR alpha; splenic haematopoiesis;
                                                             (GETH ) GENENTECH INC
                                                                                                                                        15-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                  PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN
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                                                                                  97US-0038839
97US-0049818
                                                                                                                   97US-0957063
                                                                                                                                                                                                                                                                                                                 Protein;
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62.7%;
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                                          Klein
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61;
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Query Match
Best Local Similarity
Matches 261; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Column 97-102; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acid molecule encodes a neurturin receptor-alpha amino acid sequence excluding the N-terminal signal peptide -.
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                                                                                                                                     PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 344
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62.7%;
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Search completed: December 27, 2000, 10:53:25 Job time: 116 sec

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Listing first 45 summaries
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Perfect score:
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
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length: 2000000000
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/cgn2_6/ptcdata/2/laa/5B_COMB.pep:*
/cgn2_6/ptcdata/2/laa/6_COMB.pep:*
/cgn2_6/ptcdata/2/laa/FCTUS_COMB.pep:*
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US-07-940-861-43
L US-08-459-512-43
TIS-08-459-657-43
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US-08-494-574-11

US-08-484-438-10

US-08-957-063-16

US-08-957-063-16

US-08-957-266-23

US-08-470-299-4

PCT-US96-10043-9
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Compugen Ltd
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243.533 Million cell updates/sec
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                                                                                                                                                         APPLICATION UNMBER: US 07/798,564
FILING DATE: 26-NOV-1991
APPLICATION NUMBER: DE P 40 37 837.3
FILING DATE: 28-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 02481-1132-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                          TELEFAX: 202-408-4400 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                     CURRENT AFFECTION NUMBER: US/08/
APPLICATION NUMBER: US/08/
FILING DATE: 13-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 486 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Lauffer, Leander
APPLICANT: Zettlmeissel, Gerd
APPLICANT: Oquendo, Patricia
TITLE OF INVENTION: Cell-free Receptor Binding Assays,
TITLE OF INVENTION: Production and Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                           TYPE: ami
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 20005-3315
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CITY: Washington
STATE: D.C.
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                                                           amino acid
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Query Match Best Local Similarity

67.48;

Score 1510.5; DB 1; Pred. No. 1.6e-118;

Length 486;

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/385.220
FILING DATE:
CLASSTETT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08385229 Patent No. 5605690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Jacobs, Cindy A.
APPLICANT: Smith, Craig A.
                                         ATTORNEY/AGENT INFORMATION:
NAME: Wight, Christopher L.
REGISTRATION NUMBER: 31,680
REFERENCE/DOCKET NUMBER: 2503
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Method of Treating TNF-Dependent TITLE OF INVENTION: Inflammation Using Tumor Necrosis Factor Antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219 PVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEDPEEPKSCDKTHTCPPCPAPELLGGP
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                                                                                                                                     FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            292; Conservative
X: (206) 587-0606
N FOR SEQ ID NO: CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                      Washington
                                                                                                                                                                                                                                                                                                                                       U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                     Immunex Corporation
                                                                                                                                                     US/07/946,236
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; LENGTH: 518 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-385-229-4
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                                                                                                                                                                                                                                                                                                                                                                            Sequence 1:
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 287; Conserv
                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                     MEDIOM TYPE: Floppy disk
COMPOTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                      APPLICANT: Baum, Peter
APPLICANT: Goodwin, Ray
APPLICANT: Fanslow, William
APPLICANT: Gayle, Richard
TITLE OF INVENTION: No. 5457035el
TITLE OF INVENTION: OX40
                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       488 WQQGNVFSCSVMHEALHNHYTQKSLSLSPG 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           368 NSTYRVVSVLTVLHQDWLNGKDYKCKVSNKALPAPMQKTISKAKGQPREPQVYTLPPSRD
                          APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                            STREET: 51 Uni
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 LQYVKQECNRTHNRVCECKEGRYLEI-----EFCLKHRSCPPGFGVVQAGTPERNTVCK 122
                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 YYDQ--TAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSS 131
                                                                                                                                                   ZIP: 98101
                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WQQGNVFSCSVMHEALHNHYTQKSLSLSPG 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGOPREPQVYTLPPSRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELTKNQVSLTCLVKGFYPRHIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
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                                                                                                                                                                                                             51 University
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                                                                                                                                                                                                             Immunex Corporation University Street
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63.8%;
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                                          US/08/097,827
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Pred. No. 8.9e-118;
21; Mismatches 78;
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; TELEPHONE: 206-587-0730; INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS: LENGTH: 438 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein US-08-097-827-11
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Best Local S
Matches 262
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                                                                                                                                                                                                                                                             APPLICANT: Baum, Peter
APPLICANT: Goodwin, Ray
APPLICANT: Fanslow, William
APPLICANT: Gayle, Richard
TITLE OF INVENTION: No. 5783665el Cytokine Which is a Ligand
TITLE OF INVENTION: 0X40
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 280
TELECOMMUNICATION INFORMATION:
TELECHONE: 206-587-0730
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPOTED:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/494,574
                                                                                                                                                 STREET: 51 Univ
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
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                                                                                                                                                                                                                                         ADDRESSEE: Immunex Corporation STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 CDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTD--SWHTSDECLYCSPVCKELQYVKQECN 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRECQPGHGMVNRCDHTRDTLCHPCETGFYNEAVNYDTCKQCTQCNH--RSGSELKQNCT 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALPAPIEKTISKAKGQPREPQYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELPSTPTLVEPRSCDKTHTCPPCPAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDV 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCRKHTNCSVFGLLLTQKGNATHDNICSGNS--------EST------ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTQDTVCRCR-----PGTQPRQDSGYKLGVDCVPCPPGHFS--PGNNQ 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGFFSNETSSKA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1, Application US/08494574
5783665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 438;
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US-08-464-438-10
US-08-464-438-10
; Sequence 10, Application US/08484438
; Patent No. 5811098
; Patent No. 5811098 5780031
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 206-587-0730
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino acids
TYPE: amino acid
                                                                                                                           APPLICANT: Plowman, Gregory D.
APPLICANT: Culouscou, Jean-Michel
APPLICANT: Shoyab, Mohammed
APPLICANT: Siegall, Clay B.
APPLICANT: Hellstr m, Ingegerd
APPLICANT: Hellstr m, Karl E.
TITLE OF INVENTION: HER4 HUMAN RECEPTOR TÝROSINE KINASE
NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 23-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: PETKINS, PETICIA A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2806
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 22-JUN-1
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               341 PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138 PCRKHTNCSVFGLLLTQKGNATHDNICSGNS--------EST------ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   281 ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 258 SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                  STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78
                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHEDPËVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRECQPGHGMVNRCDHTRDTLCHPCETGFYNEAVNYDTCKQCTQCNH--RSGSELKQNCT 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-JUN-1995
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

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Best Local Similarity
Matches 267; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 10-NOV-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/981,165
FILING DATE: 24-NOV-1992
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/323,442
FILING DATE: 14-OCT-1994
APPLICATION NUMBER: US 08/150,704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                 373
                                                                                                                               763
                                                                                                                                                                                                                                                                                               169
883
                                                                 823
                                                                                                                                                                                               703
                                                                                                                                                                                                                                                            643 TLPQDPVKVKALEGFPRLVGPDFFGCAEPANTFLDPEEPKSCDKTHTCPPCPAPELLGGP
                                                                                                                                                                                                                                                                                                                            592 KCPDGLQGANSFIFKYADPDRECHPC--HPNC-----TQGCNGPTSHDCIYYPWTGHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          494 ENCTAE-GMVC----NHLCSSDGCWGPGPDQCLSCRRFSRGRICIE------
                                                                                                                                                253 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL
                                                                                                                                                                                                                               193 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS
                                                                                                                                                                                                                                                                                                                                                            123 RCPDGF-----FSNETSSKAPCRKHTNCSVFGLLLTQ--KGNATHDNI---CSGNS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                          83 VCECKEGRYLEIE---FCLKHRSCPPGFGVVQAGT-----PERNTVC-----K 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 QHCTAKWKTVCAPCPDHYYTDS--WHTS-DECLYC----SPVCKELQYVKQECNRTHNR 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/484,438 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                           SCNLYDGEFREFENGSICVE---CDPQCEKMEDGLLTCHGPGPDNCTKCSHFKDGPNCVE
 QGNVFSCSVMHEALHNHYTQKSLSLSPG
                QGNVFSCSVMHEALHNHYTQKSLSLSPG 400
                                                              TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
                                                                                                                               TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL
                                                                                                                                                                                               911 amino acids
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Pred. No. 9e-
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                                                                                                                                                                                                                                                                                               -----ESTQKVDKTHTCPPCPAPELLGGP 192
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Torchia, PhD., Timothy E. REGISTRATION NUMBER: 36,700 REFERENCE/DOCKET NUMBER: P1086P TELECOMMUNICATION INFORMATION: TELEPHONE: 650/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/871
FILING DATE: 9-Jun-1997
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ATTORNEY/AGENT INFORMATION:
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286 IEKTISKAKGOPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY
                                                                                                                                     432 GPRD---FYDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP
                                                                                                                                                                                                                   379 EKT---PSLPDDLSDSTSLGTSVITTCTSVQEQGL----KANNSKELSMCFTELTTNIIP 431
                                                                                                                                                                                                                                                                                            324 -- SCRGSGNMEEECE--KFLR-DFTENPCLRNAIQAFGNGTDVNVSPKGPSFQATQAPRV 378
                                                                                                                                                                                                                                                                                                                                                                           274 NCRASYQTVTS-CPADNYQACLGSYAGMIGFDMTPNYVDSSPTG---IVVSPWC----- 323
                                                                                                                                                             166 GNSESTQKVDKTHTCPPCPAPELLGGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDP 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
COMPUTER: IE
                                                                                                                                                                                                                                                                                                                                73 KQECNRTHNRVCECKEGRYLEIEF----CLKH------RSCP--PGFGVVQAGTP 115
                                                                                                                                                                                                                                                                                                                                                                                                               32 HCTAKWKTVCAPCP-DHY-------YTDSWHTSDECLYCSPVCKELQYV 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 264; Conserv
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TYPE: Amino Acid
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                                                            EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP
                                                                                EVKFNWYVDGVEVHNAKTKPREEGYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 285
                                                                                                                                                                                                                                                      ERNTVCKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHD------NICS 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: 3.5 inch, 1.44 Mb floppy IBM PC compatible SYSTEM: PC-DOS/MS-DOS
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63.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1249.5; DB
Pred. No. 1.6e-96;
3; Mismatches 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3;
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346 KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 400

549 IEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 608

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Best Local Similarity 62.7
Matches 261; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/871
APPLICATION NUMBER: 08/871
FILING DATE: 9-Unn-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 913
FILING DATE: 18-Feb-1997
ATTORNEY/AGENT INFORMATION:
NAME: TOTCChia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: p1086P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-957-063-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 650/952-9881 INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: Amino Acid
TOPOLOGY: Line
957-non
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 664 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5 inch, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
      225 PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 284
                                                                                                                                                                                                     324 -- NCRGSGNMEEECEKFLRDFTENPCLRNAIQAFGNGTDVNMSPKGPSLP----ATQAPR 377
                                                                                                                                                            115 PERNTYCKRCPDGFFSNETSSKAPCRKHTNCSYFGLLLTQKGNATHD------NIC 164
                                                                                                                                                                                                                                                                                      274 NCRASYRTITS-CPADNYQACLGSYAGMIGFDMTPNYVDSNPTG---IVVSPWC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/957,063 FILING DATE: 24-Oct-1997 CLASSIFICATION: 800
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CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                             32 HCTAKWKTVCAPCP-DHY-------YTDSWHTSDECLYCSPVCKELQYV 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                SGNSESTQKVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED 224
                                         PG---SRDPVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED
                                                                                                                      VEKT---PSLPDDLSDSTSLGTSVITTCTSIQEQGL----KANNSKELSMCFTELTTNIS 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                             55.7%; Score 1248.5; DB 3; Length 62.7%; Pred. No. 1.9e-96; ative 21; Mismatches 61; Indels

    Klein, Arnon Rosenthal, Mary A. Hynes
Neurturin Receptor

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; ORGANISM: human
US-08-897-236-23
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                                                                                                                                                                                             RESULT
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                                                                            GENERAL INFORMATION:
APPLICANT: Browne,
APPLICANT: Murphy,
APPLICANT: Chapman
                                                                                                                                            Sequence 4, Application US/08470299 Patent No. 5783181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. SEQ ID NO 23
LENGTH: 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 23, Applicated Patent No. 6075007 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 55.5%; Score 1243.5; DB 3; Best Local Similarity 73.7%; Pred. No. 2.9e-96; Matches 244; Conservative 9; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Regeneron Pharmaceuticals, Inc.
TITLE OF INVENTION: Modified Dorsal Tissue Affecting Factor and Composition
FILE REFERENCE: REG 133
CURRENT APPLICATION NUMBER: US/08/897,236A
CURRENT FILING DATE: 1997-07-17
NUMBER OF SEQ ID NOS: 23
                            APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         488
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                                                                                                                                                                                                                                                                                                                                                                                                                                      370 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 400
                                                                                                                                                                                                                                                                                                                                                                      250 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 SNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKVDKTHTCPPCPAPELL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159 RYVKVGSCFSKRSC-----SVPE-GMVCKPSKSVHLTVLRWRCQRRGGQRC--GWI 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  345 YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                548 PIEKTISKAKGOPREPOVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENN
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                                                                                                                                                                                                                                            RWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                           EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
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Clinkenbeard, Helen
Young, Peter R.
Shatzman, Allan R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/08897236F
                                                                                            Murphy, Kay E.
                                                                                                               Browne,
 No.
21
                                                                                                             Michael J
               5783181el Compounds
                                                              Helen
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                                                                                                                                                                                                                                         Sequence 9, Application PC/TUS9610043
GENERAL INFORMATION:
APPLICANT: The General Hospital Corporation
TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES
TITLE OF INVENTION: AND METHODS
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 610-270-5090 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Sutton, Jeffrey A. REGISTRATION NUMBER: 34,028 REFERENCE/DOCKET NUMBER: P310 TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5024 TELEFAX: 610-270-5090
ZIP: 02210-2804
COMPUTER READABLE FORM:
MEDIDIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/470,299
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                         161 DNICSGNSESTQKVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             221 SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 281 ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 709 SwedeLand CITY: King of Prussia STATE: Pennsylvania
                                                                                                                                                               ADDRESSEE: Fish & Date of STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 387 amino acids TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 266
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Similarity 95.8%;
                                                                                                                                                          Boston
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USA
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Pred. No. 4.3e-96;
3; Mismatches 6
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  Version #1.30
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Best Local Similarity 89.0%;
Matches 235; Conservative
                                                                                                                                                                                                                                                                                                                              Sequence 3, Ap
Patent No. 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 200154
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 442 amino acids
                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                            TITLE OF INVENTION: ITILE OF INVENTION: ITILE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA: 55
APPLICATION NUMBER: US 60/000,213
FILING DATE: 14-JUN-1995
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APPLICATION NUMBER: PCT/US96/10043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070
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NAME: Lech, Karen F.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                     APPLICANT: CATERSON, Bruce APPLICANT: HUGHES, Clare
                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        418
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                                                                 STREET: Suite 500, CITY: Washington,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: not
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                                                    COUNTRY:
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TELEX: 200154
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                                                                                       ADDRESSEE: Foley & Lardner STREET: Suite 500, 3000 K Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        FSCSVMHEALHNHYTQKSLSLSPG 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV
                                     20007-5109
                                                                                                                                                                                                                                                                                                                                               Application US/08784512
                                                        · USA
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BUETTNER, Frank
                                                                                                                                                                                                                                                                                              BARTNIK, Eckart
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                                                                         D.C.
                                                                                                                                                           An artificial recombinant substrate (rAGG and native aggreean to study the proteolyt "Aggreeanase" in cell culture systems
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                                                                                                                                                                                 study the proteolytic
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; LOCATION:
US-08-784-512-3
                                                                                                                                                                                                                                                                                                                                                 Sequence 43, App. 5547853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity Matches 228; Conserv
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FILING DATE: 18-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, PATLICIA D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 1874
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                07-940-861-43
                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                APPLICANT: WALLNER, Barbara P.
APPLICANT: MILLER, Glenn T.
APPLICANT: ROSA, MARGARATE D.
APPLICANT: ROSA, MARGARATE D.
TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE
TITLE OF INVENTION: FUNCTION ASSOCIATED ANTIGEN 3
NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 17-JAN-PRIOR APPLICATION DATA:
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                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                         STREET: 875 Third
CITY: New York
STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         286 IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     166 GNSESTQKVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 221 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161 GDPEEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS: sir
TOPOLOGY: linear
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                                                           COUNTRY: U.S.A. ZIP: 10022-6250
                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY
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                                                                                                                                      E: Fish & Neave
875 Third Avenue
                                                                                                                                                                                                                                                                                                                    BIOGEN, INC.
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IBM PC compatible
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97.0%;
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Pred. No. 7.2e-96;
2; Mismatches 5;
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US-08-459-512-43
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                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                    Sequence 43, Application US/08459512 Patent No. 5728677
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                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                           APPLICANT: BILLER, BAILLER APPLICANT: WALLINER, Glenn T.
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 875 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (212)715-0600
TELEFAX: (212)715-0673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: HALEY, James F., Jr.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 12-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION UNMEER: US 07/770,967
FILING DATE: 07-OCT-1991
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APPLICATION NUMBER: PCT/
FILING DATE: 12-MAR-1992
                                                                          APPLICANT: ROSA, MATGATET D.
TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE
TITLE OF INVENTION: FUNCTION ASSOCIATED ANTIGEN 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        199 PKPKDTIMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS 258
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nes 235; Conserv
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TELEX: 14-8367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/07/940,861 FILING DATE: 21-OCT-1992
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                                                                                                                                                                                                                                                                                                                                   CSVMHEALHNHYTQKSLSLSPG
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89.7%;
                                                                                                                                                         Barbara P.
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                                                                                                                                                                                                                                                                                                                                     346
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Pred. No. 7.3e-96;
2; Mismatches 11
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COMPUTER READABLE FORM:

10022-6250

MEDIUM TYPE:

Floppy disk

STATE: N

New York

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Matches
                                                                                                                        Patent No. 5914111
GENERAL INFORMATION:
                                                                                                                                                               Sequence 43,
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02050

FILING DATE: 12-MAR-1992

APPLICATION NUMBER: US 07/667,971

FILING DATE: 12-MAR-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/770,967

FILING DATE: 07-007-1991

FILING DATE: 07-007-1991
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TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 43:
    APPLICANT: BIOGEN, INC.
APPLICANT: WALLMER, Barbara P.
APPLICANT: MILLER, Glenn T.
APPLICANT: ROSA, Margaret D.
TITLE OF INVENTION: CD2-BINDING
TITLE OF INVENTION: FUNCTION ASS
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LENGTH: 347 amino acids
TYPE: amino acid
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REGISTRATION NUMBER: 27,774
REFERENCE/DOCKET NUMBER: B151CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)715-0600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 07-OCT-1991
ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,512
FILING DATE: 02-JUN-1995
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nes 235; Conserv
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                                                                                                                                                                                                                                                               CSVMHEALHNHYTQKSLSLSPG 346
                                                                                                                                                                                                                                                                                                                                              LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS 324
                                                                                                                                          3, Application US/08459657
ROSA, Margaret D.
VENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE
VENTION: FUNCTION ASSOCIATED ANTIGEN 3
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SYSTEM: PC-DOS/MS-DOS
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89.7%;
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2; Mismatches
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RESULT 15

US-02-400-132-43

; Sequence 43, Application US/08460132

; Patent No. 5928643

; GENERAL INFORMATION:
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Best Local Similarity
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APPLICATION NUMBER: PCT/US92/02050
FILING DATE: 12-MAR-1992
APPLICATION UNUMBER: US 07/667,971
FILING DATE: 12-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION DATA: US 07/770,967
FILING DATE: 07-0CT-1991
ATTORNEY/AGENT INFORMATION:
NAME: HALEY, James F., Jf.
REFERENCE/DOCKET NUMBER: 27,794
REFERENCE/DOCKET NUMBER: H151CIP2
TELEPHONE: (212)715-0600
TELEPHONE: (212)715-0673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (212)715-0673
TELEX: 14-8367
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CORRENT APPLICATION DATA:
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                                                                                                                                     379 CSVMHEALHNHYTQKSLSLSPG 400
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STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                         PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS
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Pred. No. 7.3e-96;
2; Mismatches 11;
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APPLICANT:

BIOGEN, INC

378 264

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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US_07/940,861
FILING DATE: 02-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US_07/940,861
FILING DATE: 12-WAR-1992
APPLICATION NUMBER: US_07/667,971
FILING DATE: 12-WAR-1992
PRIOR APPLICATION NUMBER: US_07/667,971
FILING DATE: 12-WAR-1992
PRIOR APPLICATION NUMBER: US_07/667,971
FILING DATE: 12-WAR-1991
PRIOR APPLICATION NUMBER: US_07/770,967
APPLICATION NUMBER: US_07/770,967
FILING DATE: 07-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: HALEY, James F. Jr.
REGISTRATION NUMBER: B151CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)715-0600
TELEFAX: (212)715-0673
TELEPAX: 14-8367
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
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Best Local Similarity 89.7%;
Matches 235; Conservative
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ZIP: 10022-6250
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE
TITLE OF INVENTION: FUNCTION ASSOCIATED ANTIGEN 3
NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                               153 TQKGNATHDNICSG------NSESTQK----VDKTHTCPPCPAPELLGGPSVFLFP 198
                                                                                                               319 LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS 378
                                                                                                                                                                                    205
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                                                                                                                                                                                                                                                                                                 199 PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS 258
                                                                                                                                                                                                                                                                            145 PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS
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                          CSVMHEALHNHYTQKSLSLSPG 400
  CSVMHEALHNHYTQKSLSLSPG 346
                                                                                       LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS 324
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ET: 875 Third Avenue
: New York
E: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1237; DB 2; Length 347;
Pred. No. 7.3e-96;
2; Mismatches 11; Indels 1
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Search completed: December 27, 2000, 10:53:56 Job time: 147 sec

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Result
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Maximum Match 100%
Listing first 45 s
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length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR_65:*
1: pir1:*
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2240
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Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ETFPPKYLHYDEETSHQLLC.....VMHEALHNHYTQKSLSLSPG
        B
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Compugen Ltd.
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374	397.5	566	572.5	574.5	702	755.5	766	37 777.5	777.5	777.5	791	801.5	802.5	804.5	812.5
16.7	17.7	25.3	25.6	25.6	31.3	33.7	34.2	34.7	34.7	34.7	35.3	35.8	35.8	35.9	36.3
549	572	152	249	218	180	475	327	474	405	336	322	335	446	329	469
2 S04845	2 846529	2 S14236	2 \$69340	2 A36040	2 146732	2 S01321	2 S06611	2 S25057	1 G2MSBM	1 G2MS11	2 PS0019	1 G2MSAB	2 S40295	2 S00847	2 \$37483
Ig heavy chain pre	Ig Y heavy chain (Ig gamma-1 chain C	Ig heavy chain VHI	Ig heavy chain V-I	Ig gamma heavy cha	Ig gamma-2b chain	Ig gamma-2 chain C	Ig gamma-2b chain	Ig gamma-2b chain	Ig gamma-2b chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2c chain	Ig gamma-2a chain

ALIGNMENTS

Hoppe-Seyler's 2. Physici. Chem. 33/, 13/1-1604, 19/6 A-THIND TIPE TIME THE THE TIPE TO TH	a-va chain
R; Ponstingl, H.; Hilschmann, N.	a-1 chain C
A; Note: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met	a-1 chain C
A; Moderate Cype: Process: 136-165, 'Q',156-165, 'Q',167-176, 'Q',178-194, 'N',196-197, 'D',199-238, 'E',2	a-1 chain C
A; ACCESSION: AYUOO4	nal antibod
A:Contents: Eu	a-2b, chain
A; Reference number: A90564; MUID:71064025	a-3 chain C
A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se	a-1 chain -
Biochemistry 9, 3171-3181, 1970	y chain Cr
R; Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.	y chain pre
A; Note: this sequence has the Glm(3) marker, 97-Arq	a 3 chain c
A. Rosidines: 1-96 / RY .98-135 <cun></cun>	a 2 Chain C
A; ACCESSION: 390563	a 4 Chain C
A; Contents: myeloma protein Eu	a 2a chain
A; Reference number: A90563; MUID:71064024	a 2b chain
A; Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sec	a chain Č r
	a-3 heavy c
11 . (2)	a-A Chain C
A; RESIGUES: 88-113; 235-330 <738>	a-3 chain C
A; Molecule type: DNA	
A; Accession: S33887	
A; Reference number: S33887; MUID:83001943	
A; Title: Structure of human immunoglobulin gamma yenes: implications for evolution of	a-1 chain C
	y chain V r
R; Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.	a-1 chain C
A-Cross references: EMBI-:217370	· · · · · · · · · · · · · · · · · · ·
A; MOLECULE CYPE: INA A: Residines: 2-33: AHARY	tion
A;Accession: S36861	
A; Reference number: S33904	
submitted to the EMBL Data Library, October 1992	
R; Harris, L.J.	F
A.Note: LIES sequence has the dum(1) altorypic market, 3, bys, and the dim(1) market A.Note: LYS-330 is removed after translation	printed,
A;Cross-references: EMBL:Z1/3/U	
A; Residues: 1-330 <ell></ell>	
A; Molecule type: DNA	
A; Accession: A93433	
A; ILLE: THE HUCLECULUE SEQUENCE OF A HUMAN HUMANUSCOULTH C GAMMAT YEAR. A: Reference number: A93433; MUID: 82274238	
Nucleic Acids Res. 10, 40/1-40/9, 1982	
R;Ellison, J.W.; Berson, B.J.; Hood, L.E.	
C; Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146	
C.Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text_change 16-Jul-1999	
19 gamma-1 Chain C region - numan	
GHHU	

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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E'
A; Note: this sequence has the Glm(17) and Glm(1) markers
R; Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A; Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgGl:
A; Reference number: A91723; MUID:83289131
A; Contents: myeloma protein KOL; disulfide bonds
RESULT
S72664
Ig heav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            c;Complex: An immunoglobulin heterotetramer subunit consists of two identical light hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate int c;Superfamily: immunoglobulin C region; immunoglobulin homology C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin c;20-85/Domain: immunoglobulin homology <IM1> F;20-85/Domain: immunoglobulin homology <IM2> F;137-206/Domain: immunoglobulin homology <IM2> F;137-206/Domain: immunoglobulin homology <IM3> F;27-83,144-204,250-308/Disulfide bonds: #status experimental F;103/Disulfide bonds: interchain (to light chain) #status experimental F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Cross-references: GDB:120085; OMIM:147100
A:Map position: 14932.33-14932.33
A:Introns: 99/1; 114/1; 224/1
C:Complex: An immunoglobulin heterotetramer
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Biochemistry 9, 3188-3196, 1970

tle: The covalent structure of a human gammaG-immunoglobulin. ference number: A90565, MUID:71064027

A; Contents: annotation; disulfide bonds
R; Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A; Title: Rule of antibody structure. The primary structure enbromide cleavage products, and the disulfide bridges.
A; Reference number: A91667; MUID:77070367
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A; Contents: myeloma
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A;Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330
A;Note: this sequence has the Glm(3) and Glm(non-1) markers
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                                                                                                                                                                      HYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 268
                                                                                                                                                                                                                                                                                    SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN 388
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92.1%;
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Pred. No. 1.2e-68;
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Ig gamma-1 chain C region - synthetic
C. Species: synthetic
A; Note: Homo sapiens (man) gene engineered and express
C; Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #t
C; Accession: S31866
R; Filpula, D
submitted to the EMBL Data Library, February 1993
A; Description: Screeing method for protein-protein int
A; Reference number: S31866
A; Molecule type: mRNA
A; Residues: 1-255 <FILD
Name of the protein structure of 
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C;Date: 14-Feb-1997 #sequence_revi
C;Accession: S72664
R;Khamlichi, A.A.
submitted to the EMBL Data Library
A;Reference number: S72664
A;Accession: S72664
A;Accession: S72664
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <KHAD
A;Cross-references: EMBL:x81695
C;Superfamily: immunoglobulin C re
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Best Local S
Matches 228
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Matches 226: Conserv
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#sequence_revision 17-Mar-1997 #text_change
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Pred. No. 2.5e
4; Mismatches
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Pred. No. 1.9e-68;
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g gamma chain C region - chimpanzee); Species: Pan troglodytes (chimpanzee); Date: 23-Nov-1991 #sequence_revision 23-Nov C; Accession: PT0207
R; Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28, 319-322, 1991
A; Title: Nucleotide sequence of chimpanzee Fc A; Reference number: PT0207; MUID:91287716
A; Accession: PT0207
A; Molecule type: mRNA
A; Residues: 1-234 < EHR>
C; Superfamily: immunoglobulin C region; immunoglobulin
F; 48-117/Domain: immunoglobulin homology < IMM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig heavy chain V region precursor - human
C:Species: Homo sapiens (man)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change
C:Accession: S69339
R:Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A:Title: Structure of abnormal heavy chains in human heavy-chain.
A:Reference number: S69339; MUID:95262687
A:Accession: S69339
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Matches 221
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                                                                                                                                                                                                           Superfamily: immunoglobulin C region; immunoglobulin Keywords: immunoglobulin
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Best Local Similarity
Matches 225; Conserv
                                                  170 STOKVDK------THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
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SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 280
                                SNTKVDKKVEPKSCDTTHTCPPCAAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV 60
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                                                                                                       Conservative
                                                                                                                                                                                       immunoglobulin homology < IMM>
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                                                                                                                    52.8%;
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                                                                                                   Score 1183.5; DB
Pred. No. 1.1e-65;
1; Mismatches 3
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RESULT 7
A60764
Ig gamma-3 chain C region, form LAT - hum
C; Species: Homo sapiens (man)
C; Date: 14-May-1993 #sequence_revision 14
C; Accession: A60764
R; HuCk, S; Lefranc, G; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14432.33-14432.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobuC;Keywords: immunoglobulin
E;20-85/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefra Nucleic Acids Res. 14, 1779-1789, 1986
A:Title: Sequence of a human immunoglobulin gamma 3 heavy A;Reference number: A23511; MUID:88148507
A;Accession: A23511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-377 <HUC>
A; Cross-references: GB:X03604; GB:M12958; NID:g33070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: GDB: IGHG3
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C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                    AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 300
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                                                                                                                                                                                                       YSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPG
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Pred. No. 1e-63;
9; Mismatches
                                                              14-мау-1993
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A; Molecule type: DNA
A; Residues: 1-326 <ELL>
A; Residues: 1-326 <ELL>
A; Note: Lys-326 is probably removed posttranslationally
R; Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A;Molecule type: protein
A;Residues: 1-24, E',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198
A;Note: this sequence_has since been revised
                                                                                                                                                                        A; Molecule type: protein
A; Residues: 1-19,'0,'21-57,'z',59,'A',61-193,'D',195-325 <WAN>
A; Residues: 1-19,'0,'21-57,'z',59,'A',61-193,'D',195-325 <WAN>
A; Note: Trp-156 is at or near the complement-binding site
R; Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change
C;Accession: A93906; A92809; A90752; A93132; A02148
                                                                                      A; Title: The amino acid sequences of the three A; Reference number: A90752; MUID: 80001357 A; Contents: myeloma protein Zie A; Accession: A90752
                                                                                                                                                                                                                                                                                                              A;Title: The primary structure of a human A;Reference number: A92809; MUID:81007873 A;Contents: myeloma protein Til
                                                                                                                                                                                                                                                                                           A; Accession:
                                                                                                                                                                                                                                                                                                           A; Contents: myeloma protein
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A; Residues: 1-377 <HUC>
C; Superfamily: immunogl
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A;Accession: A60764
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: A93906;
A;Accession: A93906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEILISON, U.; Hood, L.
CELLISON, U.; Hood, L.
COC. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
OC. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
Title: Linkage and sequence homology of two humanical managements and sequence homology of two humanical managements and sequence homology.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 360
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Pred. No. 1.46
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                                                                                                                                                        heavy chain
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A;Title: Nucleotide sequence of a human in A;Reference number: A90933; MUID:83157104 A;Accession: A90933 A;Molecule type: DNA

R;Ellison, J.; Buxbaum, J.; DNA 1, 11-18, 1981

Ig gamma-4 chain C region human
C;Species: Homo sapiens (man)
C;Date: 02-Apr-1982 #sequence_revision
C;Accession: A90933; A90249; A02150

02-Apr-1982

#text_change 16-Jul-1999

immunoglobulin

C-gamma4

G4 HU

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A; Cross references: GDB:119338; OMIM:147110
A; Cross references: GDB:119338; OMIM:147110
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical C; Complex: An immunoglobulin heterotetramer subunit consists of two identical hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associated by the subunit consists of two identical c; Superfamily: immunoglobulin C region; immunoglobulin homology C; Seywords: duplication; glycoprotein; heterotetramer; immunoglobulin f; 20-85/Domain: immunoglobulin homology <IM1>
F; 133-202/Domain: immunoglobulin homology <IM2>
F; 239-306/Domain: immunoglobulin homology <IM3>
F; 27-83,140-200,246-304/Disulfide bonds: status experimental f; 102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental f; 102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental f; 176/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy of A;Reference number: A90253; MUID:72033500
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A; Contents: annotation; Zi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Hofmann, T.; Parr, D.M. submitted to the Atlas, March
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: A93132; A; Contents: Zie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: GDB: IGHG2
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C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein A; Residues: 238-275 < HOF>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mol. Immunol. 16, 923-925, 1979
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Best Local S
Matches 214
149
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les 214; Conservative
                                                                                                                                                                                                                                                   APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN
                                                                                                                                                                                      DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP
                                                                                    APIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN
                                                                                                                                                                     DPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLP
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MUID:80114419
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Pred. No. 2e-63;
8; Mismatches
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associate into
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Ig gamma-3 heavy chain disease proteins - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999
C;Accession: A90442; A90219; A90199; A93915; A02149
R;Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C.
Biochemistry 19, 4304-4308, 1980
A;Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy-A;Reference number: A90442; MUID:81021548
A;Contents: heavy chain disease protein Wis
A;Accession: A90442
A;Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain A;Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain A;Note: the sequence of residues 42-76 was taken from the reference that follows
A;Note: the sequence of residues 42-76 was taken from the reference that follows
R;Michaelsen, T.E.; Frangione, B.; Franklin, E.C.
J. Biol. Chem. 252, 883-889, 1977
A;Reference number: A92219; MUID:77118561
A;Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein W
A;Accession: A92219
A;Maccession: A92219
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A; Note: the sequence was determined from the germline gener, Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, (Biochem. J. 117, 33-47, 1970
A; Title: Human immunoglobulin sublclasses. Partial amino a A; Reference number: A90249; MUID:70207560
A; Accession: A90249
A; Molecule type: protein
A; Residues: 1-30;81-326 <PIN>
C; Genetics:
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A;Cross:references: GDB:119340; OI
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 111/1; 221/1
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34-203/Domain: immunoglobulin homology <IM2>
34-203/Domain: immunoglobulin homology <IM3>
40-307/Domain: immunoglobulin homology <IM3>
40-307/Domain: immunoglobulin homology <IM3>
40-307/Domain: immunoglobulin homology <IM3>
40-307/Domain: immunoglobulin homology <IM3>
240-307/Domain: immunoglobulin homology <IM3>
240-307
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212; Conserv
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Pred. No. 1
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1.2e-62;
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Ig gamma chain C region - rabbit C; Species: Oryctolagus cuniculus (domestic rabbit) C; Species: 07yctolagus cuniculus (domestic rabbit) C; Date: 24-Apr-1984 #sequence_revision 15-Nov-1984 ## C; Accession: A91749; A90290; A93928; A90245; A94416; R; Bernstein, K.E.; Alexander, C.B.; Mage, R.G. Immunogenetics 18, 387-397, 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin C region; immunoglobulin; pyroglutamic acid C;Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid C;Keywords: immunoglobulin homology <IMM>
F;10/3-270/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental F;6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein
A; Residues: 59-125, 'EB', 128-226, 228-289 <WOL>
A; Residues: 59-125, 'EB', 128-226, 228-289 <WOL>
A; Note: this protein lacks most of the V region, all of the CH1 re
R; Alexander, A.; Steinmetz, M.; Barritault, D.; Frangione, B.; Fra
Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A; Title: gamma heavy chain disease in man: cDNA sequence supports
A; Reference number: A93915; MUID:82247835
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A;Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, R;Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, Biochem. Biophys. Res. Commun. 71, 907-914, 1976
A;Title: The amino acid sequence of "heavy chain disease" prod A;Reference number: A90198; MUID:77021516
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A; Residues: 12-70;72-114;116-125,'E',127-133,'L',135-136,'E',138,'Y',140-154,'D',156.
A; Residues: 12-70;72-114;116-125,'E',127-133,'L',135-136,'E',138,'Y',140-154,'D',156.
A; Note: a carboxyl-terminal Lys is removed posttranslationally
A; Note: this sequence may represent an allelic form or another gamma chain subclass
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A; Note: the hinge region
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                                                                                                                                                                                                                                                                                                                                                                                                            VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA 332
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218; Conserv
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70.8%;
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Pred. No. 1.5e-62;
9; Mismatches 22;
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6; A02161
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A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 129-131;155-172,'D',174-184,'A',186,'E',188-200,'D',202-217,'E',219-232,'Q',
A; Note: this has the e15 allotypic marker, 185-Ala
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into li
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F; 20-82/Domain: immunoglobulin homology <IMI>
                     RESULT
I47160
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A;Accession: A91749
A;Molecule type: mRNA
A;Residues: 1-323 <BER>
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A; Residues: 132-143, 'E',145-161 <FRU>
R; Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.I
in Gamma Globulins, Nobel Symp. 3, Killander,
A; Reference number: A94416
A; Accession: A94416
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a; Molecule type: mRNA

asidues: 88-103; /m',105-143, 'E',145-184, 'A',186, 'E',188-266 < MAR>

oss-references: GB:M16426; NID:g165111; PIDN:AAA31289.1; PID:g165112

A; Mole: this sequence has the dil allotypic marker, 104 Met, and the el5

R; Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.

Biochem. J. 116, 249-299, 1970

A; Title: Sequence studies of the Fd section of the heavy chain of rabbit A; Reference number: A90245; MUID:70110015

A; Accession: A90245; MUID:70110015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, I
Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982
A;Title: Heavy chain genes of rabbit IgG; isolation
A;Reference number: A93928; MUID:83299917
A;Accession: A93928
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Biochem. J. 151, 337-349, 1975
A;Title: Sequence studies on the constant region
A;Reference number: A90290; MUID:76135469
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A; Residues: 1-47,'E',49-71,'PV',72-128 <PRA>
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                                         12
   2b
                                                                                                                  DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                               ---HTC---PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
                                                                                                                                                                                                                                                                                                                                                                                                                                          RCPDGFFS----NETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKVDKT 177
                                                                                                DSDGSYFLYNKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPG
                                                                                                                                                                         ARGOPLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPAVL
                                                                                                                                                                                             AKGOPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL 352
                                                                                                                                                                                                                                                    VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 292
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Pred. No. 1.2e-49;
3; Mismatches 46
 pig
   (fragment)
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er, J., ed., pp.109-127,
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HTCPPCP----

-APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW

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A;Gene: IgG2a C;Superfamily: immunoglobulin C region; immunoglobulin F;133-202/Domain: immunoglobulin homology <IMM>
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C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change
C;Accession: I47160
R;Kacskovics, I; Sun, J; Butler, J.E.
J. Immunol: 153, 3565-3573, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Superfamily: immunoglobulin C region; in F; 133-202/Domain: immunoglobulin homology
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                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-328 < KA
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A; Residues: 1-328 < KAC>
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;Species: Sus scrofa domestica (domestic pig)
;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997
                                                                                              Query Match
Best Local
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Immunol. 153, 3565-3573, 1994
                                    125 PDGFFSNETSSKAPC----RKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKVDK---T 177
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59
                                                                                              Local Similarity
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PSGLYSLSSMYTVPASSLSSKSYTCNV---
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                                                                                            Score 917.5; DB 2
Pred. No. 2.6e-49;
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Pred. No. 2.6
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G2GP

Ig gamma-2 chain C region - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 07-May-1981 #sequence_revision 07-
C;Accession: A94553; A90352; A90359; A9031
R;Trischmann, T.M.
submitted to the Atlas, April 1975
A;Reference number: A94553
A;Accession: A94553
A;Accession: A94553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: IgG4
C;Superfamily: immunoglobulin C
F;82-151/Domain: immunoglobulin
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A; Residues: 1-277 <KAC>
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C:Species: Sus scrofa domestica (domestic pig)
Nate: 21-Feb-1997 *sequence_revision 21-Feb-1997
Accession: 147162
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol, 153, 3565-3573, 1994
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Matches 176
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VDGTYFLYSKLAYDKASWQRGDTFQCAVMHEALHNHYTQKSIFKTPG
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                                                             on 07-May-1981 #text_change
A90384; A90385; A02151
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R;Trischmann, T.M.; Cebra, J.J.

Biochemistry 13, 4804-4811, 1974
A;Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodic A;Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodic A;Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodic A;Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodic A;Reference number: A90385; MUID:75036073

A;Accession: A90385
A;Molecule type: protein
A;Reference number: A90354; MUID:71058474
A;Cochenistry 10, 26-31, 1971
A;Title: Interchain disulfide bonds
A;Note: Cys-16 is involved in a heavy-light chain bond
A;Note: Cys-16 is involved in a heavy-light chain bond
A;Note: Cys-16 is involved in a heavy-light chain bond
C;Comment: This chain was isolated from pooled serum of strain I3 inbred guinea pigs
C;Complex: An immunoglobulin heterortetramer subunit consists of two identical light chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into c;Superfamily: immunoglobulin C:region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterortetramer; immunoglobulin
F;21-81/Domain: immunoglobulin homology <IM1>
F;21-81/Domain: immunoglobulin homology <IM2>
F;21-308/Disulfide bonds: #status experimental
F;178/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;178/Binding site: carbohydrates experimental
F;178/Binding site: carbohydrates experimental
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A; Molecule type: protein
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Biochemistry 13, 4796-4803, 1974.
B:Title: Primary structure of the C-H2 homology region from A;Reference number: A90384; MUID:75036072
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Biochemistry 10, 9-17, 1971
A; Title: Structure of heavy
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"The covalent structure of a human Intrachain disulfide bonds.";

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	DISULFIDE BONDS. Hilschmann N.; Ination of antibod immunoglobulin I 4:713-747(1983).	e primary structure loma protein Nie). n, alignment of the lete structure."; 7:1571-1604(1976).	Bennett C., Konigsberg Han gamma G-immunoglobul Inogen bromide fragments	(EU). all W.E., Gottlieb P. gamma G-immunoglobul gen bromide fragments	; immunoglobulin C).	Vertebrata; E i; Hominidae;	updat n upd	ALIGNMENTS RT: 330 AA.	TER IT TER TER TER OK UK MAN MAN MAN
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Biochemistry 20:3361-2370(1981).

-!- MISCELLANEOUS: NIE HAS THE G1M(17) ALLOTYPIC MARKER, 97-K, & THE G1M(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE G1M(3)

MARKER & THE G1M (NON-1) MARKERS.

-!- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF 35,116,198,269 & 272.
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Rule of antibody structure. The primary structure of a monoclonal 1961 immunoglobulin (myeloma protein Nie), I: Purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";
Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
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               Ellison J.W., Hood L.E.;
"Linkage and Sequence Homology of heavy chain constant region genes. Proc. Natl. Acad. Sci. U.S.A. 79:1
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Pred. No. 7e-77;
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REVISIONS TO 25; 5
Hofmann T., Parr I
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MEDLINE; 72033500.
MILSTein C., Frangione B.;
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MEDLINE; 95255298.
Stoppini M., Bellotti V., Neg
"Characterization of the two
immunoglobulins.";
                                                                                                                                                                                           EMBL; V00554; CAA23814.1;
EMBL; V00554; CAA23815.1;
EMBL; V00554; CAA23816.1;
EMBL; V00554; CAA23817.1;
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J. Immunol. 125:1048-1054(1980).
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Connell G.E., Parr D.M., Hofmann T.;
"The amino acid sequences of the three
domains of a human IgG2 myeloma protein
Can. J. Biochem. 57:758-767(1979).
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MEDLINE; 80114419.
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16:923-925(1979).
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GC4_HUMAN STANDARD; PRT; 327 AA ID GC4_HUMAN STANDARD; PRT; 327 AA AC P01861; DT 21-UUL-1986 (Rel. 01, Created) DT 21-UUL-1986 (Rel. 01, Last sequence update) DT 15-JUL-1999 (Rel. 38, Last annotation update) DE IG GAMMA-4 CHAIN C REGION.
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between the Swiss Institute of Bioinformatics and the EMBL
the European Bioinformatics Institute. There are no restrict
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MICHAelsen T.E., Frangione B., Franklin E.C.;

"Primary structure of the 'hinge' region of human IgG3. Probable guadruphication of a 15-amino acid residue basic unit.";

J. Biol. Chem. 252:883-889(1977).
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SEQUENCE FROM N.A. (DISEASE MEDLINE; 82247835.
Alexander A., Steinmetz M., Franklin E.C., Hood L., Buxb
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                     Wolfenstein-Todel C., Frangione B., Prelli F., Frangione B., Prelli F., Frangione B., Prelli F., Frangione B., Prelli F., Frangione acid sequence of 'heavy chain disease' Structure of the Fc fragment of immunoglobulin G3 Structure of the Fc fragment of immunoglobulin G3 Structure Biophys. Res. Commun. 71:907-914(1976).
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"Gamma Heavy chain disease in man: cDNA sequence supports partial gene deletion model.";
Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).

-i- SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11 NORMALLY PRESENT IN THE HINGE REGION.

-i- MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN.

-i- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
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REF.2.

RISCELLANEOUS: DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION.

AND ALL OF THE CHI REGION.

MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL OF THE CHI REGION, AND PART OF THE HINGE COMPARED WITH NORMAL GAMMA-3 HEAVY CHAINS.

MISCELLANEOUS: DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM OR ANOTHER GAMMA CHAIN SUBCLASS.

MISCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR MISCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS THREE TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE
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T -> A (IN OMM).
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S -> N (IN OMM). INTERCHAIN INTERCHAIN INTERCHAIN MISSING (IN ZUC) /FTId=VAR_003895 F -> Y (IN OMM) REMOVED POST-TRANSLATIONALLY
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P01870;
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"Sequence studies on the constant region of immunoglobulin G of different allotype.";
Biochem. J. 151:337-349(1975).
                                                                                                                                                                                                                MEDLINE; 83299917.

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"Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma heavy chain and identification of two genomic C gamma genes.";

Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                            MEDLINE; 70110015.
Fruchter R.G., Jackson S.A., Mole L.
"Sequence studies of the Fd section
immunoglobulin G.";
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                                                       116:249-259(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289
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              AND 155-322
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L9; Mismatches
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heavy
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                                                                                                         the
                                                                                                    Porter R.R.;
the heavy chain
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                                                                                                                                                                                                                                                                                                                                                                                                                               of rabbit
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PIR; A0216
INTERPRC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gamma globulins, Nobel symp. 3, pp.10; Stockholm (1967).
-i- MISCELLANEOUS: REF.1 SEQUENCE HAS: 104-THR, AND THE E14 MARKER, 185-MARKERS AND REF.5 THE E15 MARKER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hill R.L., Lebovitz (In) Killander J. (e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00290;
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                                                                                                                    , M16426; AAA31289.1;
A02161; GHRB.
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                                                                                                                                                                                       ARGOPLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPAVL
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177; Conserv
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90; IG
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                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 923; DB
Pred. No. 7.4e
33; Mismatches
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> A (IN B15 MARKER).
> E (IN REF 2).
> VPV (IN REF 2).
> VPV (IN REF 3 AND 4).
> E (IN REF 3 AND 5).
> E (IN REF 5 3 AND 5).
> D (IN REF 5).
- Q (IN REF 5).
- Q (IN REF 5).
- O (IN REF 5).
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NI)
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D11 AND
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Best Local Similarity
Matches 173; Conserv
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Oliveira B., Lamm M.E.;
Oliveira B., Lamm M.E.;
"Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
Biochemistry 10:26-31(1971).
Biochemistry 10:26-31(1971).

HISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tracey D.E., Cebra J.J.; "Primary structure of the CH2 homology region from antibodies.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Structure of heavy chain Q.Z., Cebra J.J.;
"Structure of heavy chain from strain 13 guinea immunoglobulin-G(2). 3. Amino acid sequence of thalf-cystine joining heavy and light chains.";
Biochemistry 10:18-25(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Last sec
15-JUL-1999 (Rel. 38, Last an
IG GAMMA-2 CHAIN C REGION.
Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 227-311.
MEDLINE; 75036073.
Trischmann T.M., Cebra J.J.;
"Primary structure of the CH3 homology region from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 134-226.
MEDLINE; 75036072.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae;
                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibodies."
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                                                                                                                                                                                                                                                                                                                                                                                                      Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFIDE BONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochemistry 13:4804-4811(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochemistry 13:4796-4803(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Structure of heavy chain from strain 13 guinea immunoglobulin-G(2). II. Amino acid sequence of and hinge region cyanogen bromide fragments."; siochemistry 10:9-17(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 69-133 AND 312-329
                                       127
  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 INBRED GUINEA PIGS
A02151; G2GP.
                            GFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKVDKT------
                                                                                                                                                                                                                                                                                                                                                                                                                          PS00290;
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(APR-1975)
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60.3%;
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                                                                               Score 904.5; DB 1;
Pred. No. 1.4e-54;
0; Mismatches 53;
                                                                                                                                                                                                                                                                       INTERCHAIN
INTERCHAIN
INTERCHAIN
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HTIW)
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H A HEAVY CHAIN).
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                                                                                                                          329;
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                                                                                 31;
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RESULT
GC3_MOUSE
ID GC3_MOUSE
P22436;
P22436;
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Best Local Similarity
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDILINE; 85027161.
Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
Tucker P.W., Blattner F.R.;
"Structural analysis of the murine IgG3 constant region gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
IG GAMMA-3 CHAIN C REGION, SECRETED FORM.
                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBO J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
Eukaryota; Metazoa; (
                                                                                                                                                                                                                                                                                                          EMBL; J00451; -; NOT_ANNOTATED_CDS. PIR; B02156; G3MSC.
                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria;
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                                                                                                                                                                                                                                  Alternative splicing.
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                                                                                                                                                                                                                                                                                   INTERPRO;
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                     167 NSESTQKVD----KTHTCP--PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 KPVGNAETKPRVEQYNTTFRVESVLPIQHQDWLRGKEFKCKVYNKALPAPIEKTISKTKG
89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD
                                                            --HTCPPCPAPELLGGPSVFLFFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
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KTELIKRIEPRIPKPSTPPGSSCPPGNILGGPSVFIFPPKPKDALMISLTPKVTCVVVDV
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                                               YGALSSGV--
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                                                                                                                                                                                                                                                           PS00290; IG_MHC;
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114
224
329
                                                                                                Conservative
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                                               RTVSSVLQSGFYSLSSLVTVPSSTWPSQTVI--
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113 H
223 C
327 C
36228 MW;
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Rodentia;
                                                                                                          37.8%;
                                                                                                                                                                                                                                                Glycoprotein;
                                                                                              Score 847.5;
Pred. No. 9.7e
47; Mismatches
                                                                                                                                                                        CH2.
CH3.
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HINGE.
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                                                                                                                                                                                                                                                  Transmembrane;
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j.7e-51;

72;
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                                                                                                                      DB 1;
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                                                -CNVAHP--
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NON TER 1
DISULFID 15
DISULFID 27
DISULFID 106
DISULFID 109
DISULFID 119
DISULFID 119
DISULFID 112
DISULFID 112
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DISULFID
SEQUENCE
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01-FEB-1991
15-JUL-1999
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P20761;
                                                                                                                                                                                                                                                                                                                                                                                                    INTERPRO; IPRO
PFAM; PF00047;
                                                                                                                                                                                                                                                                                                                                                                                                                         "Evolution of the rat immunoglobulin gamma heavy-chain gene family."; gene 74:473-482(1988).
PIR; PS0018.
INTERPRO; IPR000495; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE; 89232738.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IG GAMMA-2B CHAIN C REGIRATUS norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                    167
                                                                                                                                107
                                                                                                                                                   181
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                     355
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                                                                                                                                                                         66
                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -FEB-1991 (Rel. 17, Created)
-FEB-1991 (Rel. 17, Last sequence update)
-JUL-1999 (Rel. 38, Last annotation update)
GAMMA-2B CHAIN C REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      œ
                  DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                  GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
                                                                                             GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
                                                                                                                             PTCPTCHXCPVPELLGGPSVFIFPKPKDILLISQNAKVTCVVVDVSEEEPDVQFSWFVN
                                                                                                                                        P-----PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
                                                                                                                                                                       SSVTSSTWPSQTVT-CNV-----
                                                                                                                                                                                             SNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKVDKT------HTC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEDDPDVHVSWFVDNKEVHTAWTQPREAQYNSTFRVVSALPIQHQDWMRGKEFKCKVNNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
DGSFFMYSKLNVERSRWDSRAPFVCSVVHEGLHNHHVEKSISRPPG
                                         GLVRKPQVYVMGPPTEQLTEQTVSLTCLTSGFLPNDIGVEWTSNGHIEKNYKNTEPVMDS
                                                                                  NVEVHTAQTQPREEQYNSTFRVVSALPIQHQDWMSGKEFKCKVNNKALPSPIEKTISKPK
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                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                              IPR003006; -.
                                                                                                                                                                                                                                                                      253
333 AA;
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106
109
112
115
147
                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                          37.6%;
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                                                                                                                                                                                                                                                                       MW;
                                                                                                                                                                                                                  38;
                                                                                                                                                                                                                 Score 843; DB 1
Pred. No. 2e-50;
8; Mismatches
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INTERCHAIN
INTERCHAIN
INTERCHAIN
                                                                                                                                                                                                                                                                                                                                                           INTERCHAIN
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                                                                                                                                                                                                                                      DB 1; Length 333;
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CHAIN)
CHAIN)
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4.
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RESULT 9
GC3M_MOUSE - STAN
AC P03987;
AC P03987;
DT 23-CCT-1986 (Rel. 0)
DT 01-AUG-1991 (Rel. 1)
DT 15-JUL-1999 (Rel. 3)
DE IG GAMMA-3 CHAIN C
OS Mus musculus (Mouse
OC Eukaryota; Metazoa;
RN [1]
DT 15-JUL-1998 (Rel. 3)
RA WEBLINE; 85027161.
RA WELS J.A., WOR'D (C.)
RA WELS J.A.
RA WELS J.A.
RA WELS J.A.
RA WORLLIE (C.)
RA WELS J.A.
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Best Local Similarity
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EMBL; V01526; CAA24767.1;
PIR; A02155; G3MSM.
INTERPRO; IPR000495; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic Acids Res. 11:6775-6785(1983).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IG GAMMA-3 CHAIN C
                                                                                                                                                    167
                                                                                                                                                                                                                                                      107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mmunoglobulin domain;
                                                                                                                                                                                                       42
                       SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 280
                                                                                                                                                                                                    YGALSSGV---RTVSSVLQSGFYSLSSLVTVPSSTWPSQTVI-----CNVAHP---AS 88
SEDDPDVHVSWFVDNKEVHTAWTQPREAQYNSTFRVVSALPIQHQDWMRGKEFKCKVNNK
                                                                                                                          NSESTQKVD----KTHTCP--PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
                                                                                                                                                                                                                                                    FGVVQAGTPERNTVCKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSG 166
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84041483.
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19, Last sequence update)
38, Last annotation update)
C REGION, MEMBRANE-BOUND FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                              37.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
E -> G (IN REF. 2).
E -> Q (IN REF. 2).
P -> F (IN REF. 2).
CF7F264B50A41B95 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CH1.
HINGE.
CH2.
CH3.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                              Score 841.5; DB 1
Pred. No. 3.1e-50;
                                                                                                                                                                                                                                                                                                         Mismatches
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; Murinae; Mus
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P01868;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
30-MAY-2000 (Rel. 39, Last annotation
IG GAMMA-1 CHAIN C REGION.
                               EMBL; V00793; CAA24172.1; --
EMBL; V00793; CAA24173.1; --
EMBL; V00793; CAA24174.1; --
EMBL; V00793; CAA24175.1; --
EMBL; V00795; CAA24176.1; --
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Obata M., Yanawaki Kataoka Y., Takahashi N., Kataoka T., Shimizu A., Obata M., Yesidman J.G., Peterlin B.M., Leder P., Honjo T.;

"Immunoglobulin gamma I heavy chain gene: structural gene sequences cloned in a bacterial plasmid.";

Gene 9:87-97(1980).
           PIR;
                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content
                                                                                                                                                                                            Svasti J., Milstein C.;
"The disulphide bridges of a mouse immunoglobulin G1 protein.";
Biochem. J. 126:837-850(1972).
                                                                                                                                                                                                                                                                                murine myeloma
J. Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 80012837.

Rogers J., Clarke P., Salser W.;

"Sequence analysis of cloned cDNA encoding heavy chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 80045036. Homjo T., Obata M.,
                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                 modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                               SEQUENCE (MYELOMA PROTEIN MOPC MEDLINE; 78242288.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning and complete nucleotide gamma 1 chain gene."; Cell 18:559-568(1979).
                                                                                                                                                                                                                                              MEDLINE;
                                                                                                                                                                                                                                                                               "Evolution of immunoglobulin subclasses. murine myeloma gammal chain."; J. Biol. Chem. 253:6068-6075(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 70-322 FROM N.A. (MYELOMA
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Takahashi N., Mano Y.;
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NTERPRO;
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IPR000495;
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Rodentia;
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Best Local Similarity
Matches 144; Conser
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p20759;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence upda
15-JUL-1999 (Rel. 38, Last annotation up
IG GAMMA-1 CHAIN C REGION.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata;
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INTERPRO;
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PIR; PS0017; PS0017
 DOMAIN
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PS00290; IG_MHC; 1.
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Rodentia;
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Mus musculus (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Eukaryota; Metazoa; Rodentia;
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21-JUL-1986 (Rel. 01, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
IG GAMMA-1 CHAIN C REGION, MEMBRANE-BOUND FORM.
                         Rogers J., Choi E., Souza L., Carter (Eisenberg D., Wall R.; Eisenberg ments encoding transmembrane immunoglobulin gamma chains."; Cell 26:19-27(1981).
                                                                                                                        conserved transmembrane
domain.";
                                                                                                                                              SEQUENCE OF 323-393 FROM MEDLINE; 82197626.
Tyler B.M., Cowman A.F.,
"mRNA for surface immunog
                                                                                                                                                                                                   "Cloning and complete nucleotide sequence gamma 1 chain gene.";
Cell 18:559-568(1979).
                                                                                                                                                                                                                                   Honjo T., Obata M., Ya
Takahashi N., Mano Y.;
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      SEQUENCE OF
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MEDLINE: 82115295
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Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
-1- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND SEGMENT OF MU CHAINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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PROSITE; PS00290; IG_MHC; 1.
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MGI:96446; IGH-4.
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                                                                      NNYKTIPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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Sikorav J.-L., Auffray C., Rougeon F.;
Sikorav G., Auffray C., Rougeon F.;
Sikorav J.-L., Auffray C., Rougeon F.;
Bilo/c gamma Ca heavy chain messenger RNA.";
Balb/c gamma Ca heavy chain messenger RNA.";
"""" Acids Res. 8:3143-3155(1980).
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MOD_RES
SEQUENCE
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TNTERPRO; IPR000495; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              de Preval C., Fougereau M.;
"Determination of the primary structure of a mouse gamma G2a immunoglobulin. Identification of the disulfide bridges.";
Eur. J. Biochem. 30:452-462(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PO1863:
P1-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation updat
IG GAMMA-2A CHAIN C REGION, A ALLELE.
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"Determination of the primary structure of a mouse IgG2a immunoglobulin:amino-acid sequence of the Fc fragment. Implication the evolution of immunoglobulin structure and function.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MYELOMA PROTEIN MOPC MEDLINE; 74175517.
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sequence-mediated domain transfer.";
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Yamawaki-Kataoka Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Biochem. 43:423-435(1974).
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immunoglobulin gamma 2a and gamma be exchanged between genes
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Best Local Sim
Matches 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IG GAMMA-2A currell (Mouse).
Mus musculus (Mouse).
Tharyota; Metazoa; Chordata; /
                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunoglobulin gamma chains.";

Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).

-: ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND SEGMENT OF MU CHAINS.
                                                                                                                                                                                               EMBL; J00471; AAB59661.1; ALT_INIT. PIR; A02154; G2MSAM. MGD; MGI:96443; IGH-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
01-AUG-1991 (Rel. 19, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
IG GAMMA-2A CHAIN C REGION, MEMBRANE-1
                                                                                                                                                                                                                                                                                                                                                                                                                     between
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                                                                                                                                               [NTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPG
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IPR003006; -.
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PROSITE; PS00290; IG_

Immunoglobulin domain; Immunoglobulin

_MHC; 1.

Transmembrane;

151

splicing

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region;

Glycoprotein,

INTERCHAIN

(WITH A LIGHT CHAIN).

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ID GCC

AC P2C

AC P2C

DT 01-

DT 15-

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Best Local Similarity
Matches 157; Conserv
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01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 GAMMA-2C CHAIN C REGION.
Råttus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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MEDLINE; 88166903.
MEDLINE; 88166903.
Brueggemann M., Delmastro-Galfre P., Waldmann H., Calabi F.;
"Sequence of a rat immunoglobulin gamma 2c heavy chain constant
"Sequence of a rat immunogloby to mouse gamma 3.";
region cDNA: extensive homology to mouse gamma 3.";
Eur. J. Immunol. 18:317-319(1988).
                PFAM; PF00047; ig; 3.
PROSITE; PS00290; IG_MHC; 1.
PROSITE; PS00290; IG_MHC; 1.
PROSITE; PS00290; IG_MHC; Immunoglobulin C region.
                                                                    EMBL; X07189; CAA30169.1;
PIR; S00847; S00847.
INTERPRO; IPR000495; -.
INTERPRO; IPR003006; -.
                                                                                                                                     use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isborsend.an email to license@isb-sib.ch).
                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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; Pred. No. 2.8e-48;
34; Mismatches 58;
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CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. . .) (P

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commercial
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               358
                                                                    238 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 297
  286
                              226
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REPQVYTLPPSRDELTKNQVSLfCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS
                             VFTAQTQPHEEQLNGTFRVVSTLHIQHQDWMSGKEFKCKVNNKDLPSPIEKTISKPRGKA 225
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Pred. No. 7.9e
41; Mismatches
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CH3.
INTERCHAIN (WITH A LIGHT CHAIN).
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

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O62327 mus musculu
O16042 homo sapien
O88734 mus musculu
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SEQUENCE FROM N.A. TISSUE-PLACENTA; MEDLINE; 98351569. MOTINAGA T., NAKAGAWA N., YASUDA H., TSUDA E., Higashio K.;		"Identity of osteoclastogenesis inhibitory factor (OCIF) and osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits	Kuriyama M., Kanno T., M	., Mochizuki SI., Yano K., Fuji	TISSUE-LUNG FIBROBLAST;	SEQUENCE FROM N.A.		of bone density."; Cell 89:309-%19(1997).	"Osteoprotegerin: a novel secreted protein involved in the regulation	, Boyle W.J.;	Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W., Cambbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,	., Elliott R., Colombero A., Tan HL., Trail G., Sullivan	ett L., Boone T., Shimamoto	Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang MS.,	MEDLINE; 97262071.	IDNEY;	SEQUENCE FROM N.A.	ממווומבובמ; בערוופרובמ; רמוומרפא; רמרמבווובווב; חסווובוובמפפ; חסוווס. [1]	; Metazoa; Chordata; Craniata; Vertebrata; E	Homo sapiens (Human).	11B OR OPG OR OCIF.	(OCIF) (IUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B).	ORTHODEOGRAPHIA DEGRECOE (ORTHODORINGIA INDIGETE)	(TrEMBLrel. 04, Last	1997 (TrEMBLrel. 04, Crea	O00300 PRELIMINARY; PRT; 401 AA. O00300; O60236;	TLT 1

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RT "Cloning and characterization of the gene encoding human representation of the gene encoding human state of the gene encoding human states. J. Biochem. 254:685-691(1998).

CC J. FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STACES OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY SYNTHESIZED BONE AND CARFILAGE. MAY INHIBIT IN VITRO CONTENDED TO STEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY SYNTHESIZED BONE AND CARFILAGE. MAY INHIBIT IN VITRO CONTENDED TO STEOCLAST PROGENITORS.

CC OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CCELL SIGNALING BETWEEN CO. -! SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY STROMAL CELLS AND OSTEOCLAST PROGENITORS.

CC SIMILARITY!.

CC SIMILARITY: COCATION: EXTRACELLULAR.

CC ISSUBCELLULAR LOCATION: EXTRACELLULAR.

CC SIMILARITY: CONTAINS A LA-NGFR/TOFF TYPE CYSTEINE-RICH REGION.

CC THE PANCREAS OR PERIPHERAL BLOOD LYMPHOCYTES.

CC ISSUBLIARITY: CONTAINS A LA-NGFR/TOFR-TYPE CYSTEINE-RICH REGION.

CC SIMILARITY: BAA32076.1; -.

EMBL; AB008822; BAA32076.1; -.

EMBL; AB008821; BAA32076.1; -.

DR HSSP; P25942; 1CDF.

DR HSSP; P25942; 1CDF.

DR HSSP; P25942; 1CDF.

DR HSSP; P25942; 1CDF.
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                                                              PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 240
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                                                                                                                                                                                                                                                                                      193;
                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23
23
23
107
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401
183
63
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1143
3655
3655
105
105
1160
1160
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                                                                                                                                                                                                                                                                                                    45.2%;
68.7%;
                                                                                                                                                                                                                                                                                                                                                                  WW.
                                                                                                                                                                                                                                                                                      12;
                               ----FTPNWLSVLVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                   Score 1013.5; DB 4;
Pred. No. 4.5e-81;
                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
A -> D (IN REF. 2 AND 3).
EB42FA51C9D7C71E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OSTEOPROTEGERIN.
4 X TNFR-CYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEATH DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY
                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY
 281
                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                   Length
                               NLPGTKVNA
                                                                                                                                                                                                                                                                                      39;
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                           141
                                234
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RESULT
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Best Local Sin
Matches 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9UHP4;
01-MAY-2000
01-MAY-2000
01-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
PROSITE;
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sheng Wu
EMBL; AFI
                                                                                                                                                                                                                                             01-JUL-1997 (TrembLrel. 04
01-JUL-1997 (TrembLrel. 04
01-MAY-2000 (TrembLrel. 13
OSTEOPROTEGERIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TIEMBLIEL 13, 01-MAY-2000 (TIEMBLIEL 13, 01-JUN-2000 (TIEMBLIEL 14, OSTEOPROTEGERIN (FRAGMENT)).
                                                                                                                                                                                                                                                                                                                                      O08712 PRE
O08712; O70202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
MEDLINE: 97262071.
Simonet W.S., Lacey D.L., Dunstan
Luethy R., Nguyen H.Q., Wooden S.,
                                                                                                                                  ÎNFRSF11B OR OPG.
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9UHP4
                                                                  SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-PLACENTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218
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ning and Expression of Os
g Wu Hua Hsueh Yu Sheng W
AF134187; AAF20168.1;
RPRO; IPRO01368; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETFPPKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -RIKROHSSOEOTFOLLKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AKTKPREEQYNSTYRVVSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --CGIDVTLCEEAFFRFAVPTK-**---FTPNWLSVLVD---NLPGTKVN--AESVE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YCSPYCKELQYYKQECNRTHNRYCECKEGRYLEIEFCLKHRSCPPGFGYYQAGTPERNTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pF00020; TNFR_c6; 3.
fE; PS00652; TNFR_NGFR_1;
fE; PS50050; TNFR_NGFR_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 73.4
90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             372 AA;
                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G.-Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42758 MW;
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73.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhang W.-J., Wu X.-F.;
on of Osteoprotegerin from Homo sapiens.";
Sheng Wu Wu Li Hsueh Pao 31:680-684(1999).
                                                                                                                                                                                                                                                                    04,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235
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    Created)
    Last sequence update)
    Last annotation update)
    (OSTEOCLASTOGENESIS INHIBITORY FACTOR)

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Pred. No. 4.5e
LO; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F02527A5CD01CCD3 CRC64;
                         a
  C.R., Kelley
Bennett L.,
                                                                                                                                                                                                                                                                                                                                                               401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .3; DB 4;
4.5e-81;
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    M., C
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    Chang
ne T.,
    Shimamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24;
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Derose M., Davy E., B

Campbell P., Sander S., Van

., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison P., Sander S., Van G., Tarpley J., Derby P., Lee R.,

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CCCCRRTA RACRARITA
                                                                            CARBOHYD
CARBOHYD
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DISULFID
DISULFID
DISULFID
                                                                                                                                                                                     REPEAT
REPEAT
                                                                                                                                                                                                      REPEAT
REPEAT
                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                             EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene and its expression in embryogenesis.";
Gene 215:339-343(1998).
-i- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMI
OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION
SYNTHESIZED BONE AND CATTERUFTING CELL-TO-CELL SIGNALING
OSTEOCLASTOGRAMSIS BY INTERUPTING CELL-TO-CELL SIGNALING
STROMAL CELLS AND OSTEOCLAST PROGENITORS.
                                                                                                                                                                                                                                               PROSITE; PS50017; DEATH_DOMAIN; 1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
Glycoprotein; Repeat; Cytokine; Signal.
               VARIANT
                                VARIANT
                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                             MGD; MGI:109587; Opg.
INTERPRO; IPR000488;
INTERPRO; IPR001368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-129/OLA, AND NIH MEDLINE; 98382527.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of bone density.";
Cell 89:309-319(1997).
                                                 VARIANT
                                                                   VARIANT
                                                                                               CARBOHYD
                                                                                                       CARBOHYD
                                                                                                                DISULFID
                                                                                                                        DISULFID
                                                                                                                                  DISULFID
                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                        PFAM; PF00020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Higashio K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mizuno A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Osteoprotegerin: a novel secreted protein involved in of bone density.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Suggs S.,
                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM).
SUBCELLULAR LOCATION: EXTRACELLULAR
TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN LIVER, LU
BRAIN, HEART, KIDNEY, STOMACH, INTESTINE, SKIN, CALVARIA
PLACENTA. NOT DETECTED IN SPLEEN.
DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGH LEVELS ARE DETEC
DAY 7. AT DAY 11, EXPRESSION DECREASES AND THEN INCREASES
15 TO DAY 17.
                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY:
                                                                                                                                                                                                                                                                                                               MGI:109587; OF
                                                                                                                                                                                                                                                                                                                                 AB013898; BAA28269.1;
AB013903; BAA33388.1; J
AB013899; BAA33388.1; J
AB013900; BAA33388.1; J
AB013901; BAA33388.1; J
AB013902; BAA33388.1; J
                                                                                                                                                                                                                                                                                                                         AB013900;
AB013901;
AB013902;
P25942; 1C
                                                                                                                                                                                                                                                                                                                                                                                       U94331; AAB53708
                                                                                                                                                                                                                                                                              PS00652; TNFR_NGFR_1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of the mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murakami A.,
                                                                  165
             288
                                                161
                                                                                                                                                                                                                                                                                        TNFR_c6; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W.J.;
                                                                                                                                                                                                                                                                                                                                                                                               CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
                                                                  21
401
201
201
1063
1143
201
365
62
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1178
                               165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS;
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JOINED.
JOINED.
                                                                                            DEATH DOMAIN.
BY SIMILARITY
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                    TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
    SWISS)
                                SWISS).
                                                                            POTENTIAL.
POTENTIAL.
                                                  SWISS)
                                                                 R -> P (IN
                                                                                                                                                                                                                                   OSTEOPROTEGERIN.
                                                                                                                                                                                                                         X TNFR-CYS
                                                                                                                                                                                                                                                                              UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESORPTION BY BLOCKING TERMINAL STAGES ON AND ALLOWING ACCUMULATION OF NEWLY
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             (IN
                              (IN
                                                (IN
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                                                                  STRAINS
                               STRAINS
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              STRAINS
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             129/OLA
                                                                 129/OLA
                              129/OLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tsuda
                                                129/OLA
                                                                                                                                                                                                                                                                                                                                                                                                                                           IN LIVER, LUNG, IN, CALVARIA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNALING
                                                                                                                                                                                                                                                                                                                                                                                                                 ARE DETECTED
INCREASES FRO
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RESULT
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                008727;
008727;
01-JUL-1997
01-JUL-1997
01-MAY-2000
                                                                                                                                                 Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S., Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shinamoto Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
                                                                                                                                                                                                                                                                                                                 01-JUL-1997 (TrembLrel. 04, 01-JUL-1997 (TrembLrel. 04, 01-MAY-2000 (TrembLrel. 13, OSTEOPROTEGERIN PRECURSOR (
                                                                                                                                                                                                          TISSUE-INTESTINE;
MEDLINE; 97262071.
                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
                                                                                                                                        Suggs
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 LOCATION: E
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Rodentia;
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3, Last annotation update)
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 EXTRACELLULAR.
A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
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Sciurognathi; Muridae;
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PFAM; PF00020; TNFR_c6;

U94330; AAB53707.1; P25942; 1CDF.

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Matches
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CARBOHYD
SEQUENCE
Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misr "Cloning of cDNAs encoding for anti-white pine antibody (Mab 7, its light and heavy chains) a single chain antibody (scFV)."; submitted (MAY-1999) to the EMBL/GenBank/DDBJ EMBL; AF152372; AAD40243.1; -.
                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                              O9R1A4 PRELIMINARY; PRT; 437 AA. 09R1A4; 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence up 01-JUN-2000 (TrEMBLrel. 14, Last annotation GAMMAI HEAVY CHAIN OF MAB7 (FRAGMENT).
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
DEATH DOMAIN
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Pred. No. 4.2e-69;
                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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INTERPRO; IPR00306; -.
PPAM; PP00047; ig; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
NON_TER 1 1
NON_TER 437 437
SEQUENCE 437 AA; 48142 MW; 5C3A7BE
                                          PROSITE;
PROSITE;
PROSITE;
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095407;
                                                                                                                                                                      superfamily (TR6) suppresses LiGHT-mediated
J. Biol. Chem. 274:13733-13736(1999).
EMBL; AF104419; AAD03056.1; -.
EMBL; AF134240; AAD29688.1; -.
HSSP; P25942; 1CDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Pitti R.M., Marsters S.A., Lawrence D.A., Dowd P., Huang A., Donahue C.J., Sherwood Godowski P.J., Wood W.I., Gurney A.L., Hill Goddard A.D., Botstein D., Ashkenazi A.; "Genomic amplification of a decoy receptor
                                                                                                                                                                                                                                                                                  Yu K.Y., Kwon B., Ni J., Zhai Y., Ebner R., I
"A newly identified member of tumor necrosis
                                                                                                                                                                                                                                                                                                                                                                                                            colon cancer.";
Nature 396:699-703(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; C
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01-MAY-1999 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
DECOY RECEPTOR 3.
                                                                                                            PFAM; PF00020;
                                                                                                                                                                                                                                                                                                                          MEDLINE; 99253915.
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                                                                                                                                                                                                                                                                                                                                                                  SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE; 99087326.
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                                                                                                                            INTERPRO; IPR000561; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      al Similarity 60.
                                       PS00652; TNFR_NGFR_1; UNKN
PS01186; EGF_2; UNKNOWN_1.
PS50050; TNFR_NGFR_2; 2.
    300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
  AA;
                                                                                                          TNFR_c6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
Primates;
    32679 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10,
10,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                      decoy receptor
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Pred. No. 1.1e-64;
4; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5C3A7BB3EE7D697C
    F90AEE33718449AF CRC64;
                                                                                      UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A., Roy M., Kischkel
bod S.W., Baldwin D.
Hillan K.J., Cohen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      À
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        for
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fas ligand in lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .T.,
R.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        400
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RESÖLT
Q62327
ID Q6
AC Q6
DT 01
DT 01
DT 01
DE TC
OS MC
OC EC
D 062327

D 062327;

C Q62327;

C Q62327;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-WAY-2000 (TrEMBLrel. 13, Last annotation update)

DT TUMOR NECROSIS FACTOR RECEPTOR 2 MRNA (FRAGMENT).

OS Mus musculus (Mouse).

Pukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
Q9PUSO
ID Q9
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Best Local S
Matches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bobe J., Goetz F.W.;
"A tumor necrosis factor receptor homolog is up-regulated trout (Salvelinus fontinalis) ovary at the completion of o Biol. Reprod. 0:0-0(1999).
EMBL; AF156738; AAD56428.1; -.
INTERPRO; IPR000561; -.
INTERPRO; IPR001368; -.
INTERPRO; IPR001368; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salvelinus fontinalis (Brook trout).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9PUSO;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2000 (TrEMBLrel. 14,
DECOY RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9PUS0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                   146
                                                                                                                                                                                                                                                                                                                                                            129
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                                                                                                                                                                                                                                                                                                                                                                                                   VVKQECSPSNNCECECKEGYYFNKKYEACIKHKECPPGYGANTTGTPHQDTECVQCQAGF 145
                                                                                                                                                                                                                                                                                                                                                                                                                             YVKQECNRTHNRVCECKEGRYL--EIEFCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGF 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKELQ 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 93
                                                                                                                                                                                                                                                                                                            YSEVSSAKATCLAQSNCKVGGLRVVLKGQDWHNTLCA 182
                                                                                                                                                                                                                                                                                                                                                        FSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DRYSGLSIVCDRCPPGTYLRAPCSAMRKSDCAECPNGAYTEFWNHISKCLRCS-MCAENQ 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCT 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSP 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 19.3%; Score 433; DB 4; Similarity 42.9%; Pred. No. 2.6e-30; 69; Conservative 29; Mismatches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PS00652; TNFR_NGFR_1; UNKNOWN_1
PS01186; EGF_2; UNKNOWN_1.
PS50050; TNFR_NGFR_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34037 MW;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 405.5; DB 13; Pred. No. 6.6e-28; 0; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E44C73477F05C3DF CRC64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63;
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                                                            Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Q16042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 100; Conserv
                                     MEDLINE; 913/vv...
Dembic 2., Loetscher H.,
Prockhaus M., Lesslauer
                                                                                                                                                                                                                                         016042 PRELIMINARY; PRT; 439 AA.
016042; PREVIMINARY; PRT; 439 AA.
016042; O1-MOV-1996 (TrEMBLrel. 01, Created)
01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
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EMBL; X76401; CAA53981.1; -.
HSSP; P19438; INCF.
                                                                                               MEDLINE; 91370690.
                                                                                                                                                                                                                              TUMOR NECROSIS FACTOR RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 95178848.
Powell E.E., Wicker L.S.,
"Allelic variation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM; PF00020; TN
PROSITE; PS00652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-NOD
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[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERPRO; IPRO01368; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175
                                                                                                                                                                                                                                                                                                                                                                                                                                        367 NVTCIVNVCSSSDHSSQCSSQASATVGDPDAKPSASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  318 SLTCLVKGFYPSDIAVEWESN-----GQPENNYKTTP 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTAPSSSSSSLESSASAGDRRAPPGGHPQARVMAEAQGSQEARASSRISDSSHGSHGTHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TVLHQDWLNGKEYKCKVSNKALPA---PIEKTISKAKGQPREPQVYTLPPSRDELTKNQV 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VNCFILVQRKKKPSCLQRDA--KVPHVPDEKSQDAVGL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KACAPGTFSDTTSSTDVCRPHRICSILAI ---- PGNASTDAVCAPESPTLSAIPRTLYVS 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KRCPDGE: SNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DQVETRACTKQQNRVCACEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLC 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LQYVKQECNRTHNRVCECKEGRYLBIEF------CLKHRSCPPGFGVVQAGTPERNTVC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --DKTHTCP-----PCPAPELL-------GGPSV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  00020; TNFR_c6; 4.
PS00652; TNFR_NGFR_1;
PS50050; TNFR_NGFR_2;
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93
268
345
421
                                                                                                                                                                 Chordata; Craniata; Vertebrata; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48686 MW;
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                                                            Σ
                                                                                Gubler
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type 2 tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 345; DB 11;
; Pred. No. 2.2e-22;
53; Mismatches 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6C51D2CF1C4626DF CRC64;
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r necrosis
                                                                                Y.C.,
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                                                                                                                                                                                                                                               update)
                                                                                Lahm
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factor
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                                                                                H.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EQQH------LL 306
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                                                                                                                                                                                    Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor
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Best Local Similarity
Matches 107; Conser
                                                                                  Genomics 0:0-0(0).

EMBL; Y14629; CAA74969.1; JOINED.

EMBL; Y14620; CAA74969.1; JOINED.

EMBL; Y14621; CAA74969.1; JOINED.

EMBL; Y14622; CAA74969.1; JOINED.

EMBL; Y14623; CAA74969.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O88734 PRELIMINARY;
O88734;
O1.NOV-1998 (TIEMBLIEL. 08, 0
O1.NOV-1998 (TIEMBLIEL. 08, 1
O1.MAY-2000 (TIEMBLIEL. 13, 1
P80 INF-ALPHA RECEPTOR.
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Cytokine 2:231-237(1990).
EMBL; S63588; AAB19824.1; -.
HSSP; P25942; ICDF:
                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                  Characterization of the
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00652; TNFR_NGFR_1; PROSITE; PS50050; TNFR_NGFR_2; SEQUENCE 439 AA; 46090 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERPRO; IPR001368; -.
PFAM; PF00020; TNFR_c6; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNFR2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VTCVVVDVSHEDP-----EVKFNWYVDGVEVHNAK-TKPREEQYNSTYRVVSVLTVLHQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSSSLESSASALDRRAP-----TRNQPQAPGVEASGAGEARASTGSSDSSPGGHGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VNCVIMTQVKKKPLCLQREAK-----VPHLPADKARGTQGPEQQH------LLITAPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGV
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IPR001368; -.
0020; INFR_c6; 4.
ps00652; INFR_NGFR_1;
                                                                                                                                                                                                                                                                                                                                                     Segade F.,
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                                                                                                                                                                                                                                                                                             Rodriguez R., Ramos S.S., rosis Factor Receptor Gene the two Transcripts.";
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Last annotation updat
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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No. 2.8e-22;
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Gene:Genomic
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                                                                                     Query Match
Best Local S
Matches 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Sin
Matches 102;
                                                                                                                                                                                                                         domain-containing TNF receptor.";
Submitted (MAY-1998) to the EMBL/GenBank/DDI
EMBL; AF068868; AAC34583.1; -
INTERPRO; IPR000488; -
INTERPRO; IPR001368; -
IPR001368; -
PFAM; PF00020; TNFR_C66; 4.
PFAM; PF00531; death; 1.
PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50017; DEATH_DOMAIN; 1.
PROSITE; PS50017; DEATH_DOMAIN; 1.
PROSITE; PS50017; DATH_NGFR_2; 1.
SEQUENCE 655 AA; 71844 MW; 48939391C485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       075509
075509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Haridas V., Wang S., Liu D.,
Pan G., Bauer J.H., Haridas V., Wang S., Liu D.,
Vincenz C., Aggarwal B.B., Dixit V.M.;
"Identification and functional characterization
"Identification" TNF receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAY-2000 (TrEMBLrel. 13, Last annotation update)
TNFR-RELATED DEATH RECEPTOR-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50050; TNFR_NGFR_2; 3.
SEQUENCE 482 AA; 51106 MW; F6C15046B48FF83C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   309
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7 YLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 HYDEETSHQLLCDKCPPGTYLKQHCT-----AKWKTVCAPCPDHYYTDSWHTSDECLY 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SHGSHGTHVNVTCIVNVCSSSDHSSQCSSQASATVGDPDAKPSASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RDELTKNOVSLTCLVKGFYPSDIAVEWESN-----GQPENNYKTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA---PIEKTISKAKGQPREPQVYTLPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLLMLGLVNCFILVQRKKKPSCLQRDAKVPHV-PDEKSQDAVGLEQQHLLTTAPSSSSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -FLEPPKPKDTLMISRTPEVTCVVVD--VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRTLYVSQPEPTRSQPLDQEPGPSQPPSILTSLGSTPIIEQSTKGGISLPIGLIVGVTSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------GGPSV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PNGNVLCKACAPGTFSDTTSSTDVCRPHRICSILAI----PGNASTDAVCAPESPTLSAI 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PERNIVCKRCPDGFFSNETSSKAPCRKHINCSVFGLLLIQKGNATHDNICSGNSESTQKV 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CSSSCSTDQVETRACTKQQNRVCACEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEF------CLKHRSCPPGFGVVQAGT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YYDRKA--QMCCAKCPPGQYVKHFCNKTSDTVCADSDTVCADCEASMYTQVWNQFRTCLS
                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                               13.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.1%; Score 338; DB 11; Length 4 25.1%; Pred. No. 9.6e-22; tive 50; Mismatches 164; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ESSASAGDRRAPPGGHPQARVMAEAQGSQEARASSRISDS
                                                                                        44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL/GenBank/DDBJ databases
                                                                                     Score 297; DB 4; I
Pred. No. 5.4e-18;
4; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                  48939391C4852A33 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D.,
                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of DR6,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N.
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                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yu
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                                                                                        42;
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                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      death
                                      66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    279
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                                                                                           11;
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                                                                                                                                                                                                               Query Match
Best Local S
Matches 103
                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ginglymostoma cirratum (Nurse shark),

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;

Blasmobranchii; Meoselachii; Galeomorphii; Galeoidea;

Orectolobiformes; Ginglymostomatidae; Ginglymostoma.
                                                                                                                                                                                                                                                                                                                                                                   extensive somatic diversification in sharks.";
Nature 374:168-173(1995).
EMBL; U18701; AAB48195:1;
INTERPRO; IPR000495;
INTERPRO; IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation updat
NOVEL ANTIGEN RECEPTOR PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q90544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q90544
                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                          PFAM; PF00047;
PROSITE; PS002
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Flajnik M.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Greenberg A.S., Avila D., Hughes M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 95183140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-SPLEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          'A new antigen receptor gene family that undergoes rearrangement
                193
                                          412
                                                                                                   355
                                                                                                                             103
                                                                                                                                                         315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         292 KAKGQPR 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54
                                                                                                                                                                                    51 DSWHTSDECLYCS------PVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRS 102
                                                                                                                                                                                                                  Local Similarity
les 103; Conserv
                                       TRSLLNLTAVEWKSGAKY--TCTASHPPSQSTVKRVIRNQKVD-----CRQTDI----
SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE-VKFNWYVDGVEVHNAKTKPREEQYN
                                                                                                                             CPPGFGVVQAGTPERNTVCKRCPDGFFSNETS---SKAPCRKHTNCSVFGLLLTQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIKGPKR 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICS---GNSESTQKVDKTHTCPPC
                                                                                                 LPPSPEEIQSTSSATLTCLIR----GFYPDKVSVSWQKDDVSVSANVTNFPTALEQDLTFS 411
                                                                                                                                                         EEWQSGVE-YTCSAKQDQSSTPVVKRTRKARVEPTKPHLRL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TVPDNTSSARGKEDVNKT--LPNLQVVNHQ---QGPHHRHIL--KLLPSMEATGGEKSST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI----EKTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSP----GTAIF---PRP-EHMETHEVPSSTYVPKGMNSTESNSSASVRPKV-LSSIQEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED-----PEVKFNWYVDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTFSDVPSSVMKCKAYTDCLSQNLVVIKPGTKETDNVCGTLPSFSSSTS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PWPMIEKLPCAALTDRECTCPPGMFQSNATCAPHTVCPVGWGVRKKGTETEDVRCKQCAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRCPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YRHYDRATGQVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTRHENGIEKCHDCSQPC
                                                                                                                                                                                                                                                                                                                                           PS00290
                                                                                                                                                                                                                                                                                 1
19
684 AA;
                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                     - KGNATHDNICSGN---SEST-----QKVDKTHTCPPCPAPELLGGP
                                                                                                                                                                                                                                                                    18
684
75224 }
                                                                                                                                                                                                                                                                                                                                          IG_MHC; UNKNOWN_3
                                                                                                                                                                                                                            12.5%;
                                                                                                                                                                                                                                                                                    ¥.
                                                                                                                                                                                                               ; Score 280.5;
; Pred. No. 1.6e
53; Mismatches
                                                                                                                                                                                                                                                                                 POTENTIAL.
NOVEL ANTIGEN RECEPTOR.
; 2FF9D2071CDA6DFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hughes A., McKinney E.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         684
                                                                                                                                                                                                                            5; DB 13;
l.6e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                         Length 684;
                                                                                                                                                                                                                85
--
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183
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                                          458
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RESULT 14
Q9Y6Q6
ID Q9Y6Q6
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Q9UP60;
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-JUN-2000 (TrEMBLrel. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zheng S., Cao J., Cao W., Cai X., Geng L.;
"Identification and characterization of SNC73, a gene valuated in colorectal cancer."

Submitted (JUN-1998) to the EMBL/GenBank/DDBJ database:
EMBL; AF067420; AAC19365.1; -.

INTERPRO; IPR000495; -.

INTERPRO; IPR003006; -.

FPAM; PF00047; 1g; 3.

PROSITE; BS00290; IG_MHC; UNKNOWN_1.

SEQUENCE: 384 AA; 40947 MW; BA7ADC3CA5A9DD48 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNC73.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; vercue.
Eukaryota; Metazoa; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNC73 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. Zheng S., Cao J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        515
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                                                                                                                                274
                                                                                                                                                                                                                    255
                                                                                                                                                                                                                                                                                                                                                                                         115 PERNTYCKRCPDGFFSNE------TSSKAPCRKHTNCSVFGLLLTQK 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   369
                                                                                                                                                                                                                                                                                                                                                               49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13
                                                                                                                                                                                        SVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATLSKS-GNTFRPEVHLLPPPSEELAL
                                                                                                                                                                                                           RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK
                                                                                                                                                                                                                                                                                                                                 GNATHDNICSGNSESTQKVDKTHTCP----PCPAPELLGGPSVFLFPPKPK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EL-TKNQVSLTCLVKGFYPSDIAVEWESNGQ-PENNYKTTPPVLDSDGSFFLYSKLTVDK 368
                                                                                                                                                                                                                                               LSLHRPALEDLLLGSEANLTCTLTGE-RDASGVTFTWTPSSGK--SAVQGPPERDLCGCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SRWQQGNVFSCSVMHEALHN---HYTQKS
                                                                         EDWKKGDTFSCMVGHEALPLAFTQKTIDRLAG
                                                                                                  SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                NELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRVAA
                                                                                                                                                           NO-VSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLD-SDG--SFFLYSKLTVDK
                                                                                                                                                                                                                                                                                                                                                              PDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQDASGDLYTTSSQLTLPATQ- 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AEWNSDTTYSCLVGHPSLNRDLIRSTNKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EIDTENSATLMCLATNFHPAEIYVGWMANDTLLDSGYRTQVDSEKGSGSSFVTDRLRLTA 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SKSTIVSKLKVMASEWDSGTEYVCLVEDSELPTPVKASIRKANVSQMHPPKVYLLHPSTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK-GQPREPQVYTLPPSRD 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVSLLKP-PFEEIWTQQTATIVCEIV---YSDLENIKVFWQVNGVERKKGVETQNPEWSG
                                                                                                                                                                                                                                                                          -----DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
                                                                                                                                                                                                                                                                                                                                                                                                                       95;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                       -CLAGKSVTCHV-KHYTNPSQDVTVPCPVPSTPPTPSPST-PPTPSPSCCHPR
                                                                                                                                                                                                                                                                                                                                                                                                                                 12.4%;
28.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                     35;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 277.5; DB 4 Pred. No. 1.5e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        663
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                                                                                                    400
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                                                                                                                                                                                                                                                                                                                                                                                                                       61;
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MEDLINE; 98032977.
Anderson D.M., Marask
Tometsko M.E., Roux E
Galibert L.;
                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999 (TrembLrel. 12, Created)
01-NOV-1999 (TrembLrel. 12, Last sequence update)
01-MAY-2000 (TrembLrel. 13, Last annotation update
RECEPTOR ACTIVATOR OF MF-KAPPA-B PRECURSOR (TNF-RINDUCED CYTOKINE RECEPTOR) (RANK).
TNFRSF11A OR RANK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Receptor; Glycoprotein; SIGNAL 1 22 CHAIN 23 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9Y6Q6;
                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 1.
Receptor; Glycoprotein; Transmembrane; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF0182
MIM; 603499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and dendritic-cell function.";
Nature 390:175-179(1997).
-i- FUNCTION: RECEPTOR FOR A CYTOKINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM; PF00020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "A homologue of the TNF receptor and dendritic-cell function.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERPRO
165
                                                                                                                                                                   47
                                                                                                                                                                                                        20
                                                                                                                                                                                                                                                                          Local
                                                                                                                        77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS RANKL. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL). TISSUE SPECIFICITY: UBIQUITOUS EXPRESSION WITH HIGH LEVELS SKELETAL MUSCLE, THYMUS, LIVER, COLON, SMALL INTESTINE AND GLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: CONTAINS
L; AF018253; AAB86809.
                                                                                                                                                                                           CDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVC---KELQYVKQEC 76
                                       SKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKVDKTHTCPP
STDKCRPWTNCTFLGKRVEHHGTEKSDAVCSSSLPARKPPNEPHVYLP
                                                                                                                   NRTHNRVCECKEGRY--LEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGFFSNETS 134
                                                                                                                                                                 CNKCEPGKYMSSKCTTTSDSVCLPCGPDEYLDSWNEEDKCL-LHKVCDTGKALVAVVAG-
                                                                                                                                                                                                                                                Similarity 34.5
58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR001368;
                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TNFR_c6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maraskovsky
                                                                                YHWSQDCECCRRNTECAPGLGAQHPLQLNKDTVCKPCLAGYFSDAFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 616
212
233
616
195
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                                                                                                                                                                                                                                                                                                                                                        66033
                                                                                                                                                                                                                                                                        11.5%;
34.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>;</u>- >
                                                                                                                                                                                                                                                                                                                                                        WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Teepe M.C., DuBose R.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION; -.
                                                                                                                                                                                                                                                  21;
                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
BY SIM
                                                                                                                                                                                                                                                                        Score 258.5; DB 4
Pred. No. 1,2e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 X TNFR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TNFR-CYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TNFR-CYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RECEPTOR ACTIVATOR OF NF-KAPPA-B. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X TNFR-CYS.
INFR-CYS 1.
INFR-CYS 2.
INFR-CYS 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Catarrhini; Hominidae.
                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             n update)
(TNF-RELATED
                                                                                                                                                                                                                                                                                           DB 4;
                                                                                                                                                                                                                                                  82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dougall W.C., ., Cosman D.,
                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
                                       182
212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTIVATION-
                                                                                                                                                                                                                                                                                             616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADRENAL
                                                                                                                                                                                                                                                Gaps
                                                                                164
                                                                                                                                                                                                                                                  4;
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106

NHTAPRRCACTAGYHWNSDCECCRRNTECAPGFGAQHPLQLNKDTVCTPCLLGFFSDVFS NRTHNRVCECKEGRY--LEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGFFSNETS 134

165

105 76

48 77

20

Conservative

41;

Indels

113;

Gaps

17;

CDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVC---KELQYVKQEC CSRCEPGKYLSSKCTPTSDSVCLFCGPDEYLDTWNEEDKCL-LHKVCDAGKALVAV-DPG

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Query Match
Best Local S
Matches 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O35305 PRELIMINANI,
O35305; O1-JAN-1998 (TrEMBLrel. 05, Created)
O1-JAN-1998 (TrEMBLrel. 05, Last sequence update)
O1-MAY-2000 (TrEMBLrel. 13, Last annotation update)
RECEPTOR ACTIVATOR OF NF-KAPPA-B PRECURSOR (TNF-RELATED RECEPTOR) (RANK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P25942; 1CDF.
MGD; MGI:1314891; Tnf.
INTERPRO; IPR000561;
INTERPRO; IPR001368;
                                                                                                                REPEAT
REPEAT
DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
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TRANSMEM
DOMAIN
DOMAIN
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anderson D.M., Maras Tometsko M.E., Roux Galibert L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00652; TNFR.NGFR.1; UNKN
PROSITE; PS001186; EGF_2; UNKNOWN_1.
PROSITE: PS50050; TNFR.NGFR.2; 1.
Receptor; Glycoprotein; Transmembra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS RANKL.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
EMBL; AF019046; AAB86810.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 390:175-179(1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "A homologue of the TNF receptor and and dendritic-cell function.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PE/AM; PF00020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 98032977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-LIVER EPITHELIUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
  al Similarity
102; Conserv
                                                                                                                                                      A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TNFR_c6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maraskovsky
Roux E.R., J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tnfrsflla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Chordata; Rodentia;
                                                                                                                    47
69
61
113
113
1134
1170
1195
                                                                                                  66621
                      11.5%;
25.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane;
                                                                                                    W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       y E., B
Teepe
                                                                                            BY SIMILARITY.
BY SIM
                                                                                                                                                                                                                                                                                                                                              4 X TNFR-CYS.

TNFR-CYS 1.

TNFR-CYS 2.

TNFR-CYS 3.

TNFR-CYS 4.
  Score 256.5; DB 1
Pred. No. 1.8e-14;
1; Mismatches 147
                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RECEPTOR ACTIVEXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Billingsley W.L., D
g M.C., DuBose R.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   its ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTIVATOR OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
                                        11;
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                                        Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTIVATION-
                                            625
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Db	Qy	ρb	Qy	망	Qy	망	Ϋ́	뮻	Qγ
358 LLIQQGSKSIPPFQEPLEVGENDSLSQCFTGTESTVDSEGCDF 400	OPENNY	298 EDGAGVCGPVCAAGGPWAEVRDSRTFTLVSEVETQGDLSRKIPTEDEYTDRPSQPSTGSL 357	p	242ALTANIWNWVNDACSSLSGNKESSGDRCAGSHSATSSQQEVCEGILLMTREEKMVP 297	255 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 291	216 IVLLFISVVVVAAIIFGVYYRKGGK 241	195 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 254	166 STDKCKPWTNCTLLGKLEAHQGTTESDVVCSSSMTLRRPPKEAQAYLPSL 215	135 SKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKVDKTHTCPPCPAPELLGGPSV 194

Search completed: December 27, 2000, 10:52:40 Job time: 71 sec

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Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                   Database :
                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ched:
                                                                                                                                                                                                           SPTREMBL_14:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        December 27, 2000, 10:51:29; Search time 60.82 Seconds (without alignments) 615.637 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                              297973 seqs, 93374136 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-389-545-2
2179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MNKWLCCALLVLLDIIEWTT.....QKLFLEMIGNQVQSVKISCL 401
sp_organelle:*
sp_phage:*
sp_plant:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                         sp_mhc:*
                                                                                                                                                        sp_mammal:*
                                                                                                                                                                            sp_invertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                             297973
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

4 4 5 4	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
204	204	204.5	205.5	207.5	207.5	209	209.5	210.5	211.5	212	212	21.2	212.5	21.1	214.5	215.5	215.5	215.5	215.5	215.5	215.5	216	217.5	218
9.4	9.4	9.4	9.4			9.6			9.7	9.7	9.7	9.7	9.8	9.8	9.8	9.9	9.9	9.9	9.9	9.9	9.9	9.9	10.0	Ì0.0
320	283	351	326	351	351	349	350	347	326	348	348	348	347	350	360	349	349	349	349	348	348	349	349	349
12	4		12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12
057300	Q92956	057121	057122	073559	057117	057109	057123	057115	057120	057108	057103	057277	057119	057116	057118	057102	057101	057100	057291	Q85407	057112	860680	057099	Q89118
																						~		
O57300 ectromelia	homo	cowpox		073559 cowpox viru		_		O57115 cowpox viru	O57120 cowpox viru	O57108 monkeypox	-	-					O57101 monkeypox	_	057291 monkeypox	Q85407 variola vir	variola	Q89098 variola vir	057099 monkeypo	Q89118 variola vir

ALIGNMENTS

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CARBOHYD
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50017; DAATH_DOMAIN; 1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
Glycoprotein; Repeat; Cytokine; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
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EMBL;
                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                         VARIANT
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PFAM; PF00020;
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                                                                                                                                                                                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP;
         181
                         121
                                           121
                                                           61
                                                                           61
                                                                                          SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE L; U94331; AAB53708.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN LIVER, LUNG, PRAIN, HEART, KIDNEY, STOMACH, INTESTINE, SKIN, CALVARIA AND PLACENTA. NOT DETECTED IN SPLEEN.
DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGH LEVELS ARE DETECTED DAY 7. AT DAY 11, EXPRESSION DECREASES AND THEN INCREASES FR. 15 TO DAY 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGI:109587; Opg.
RPRO; IPR000488; -.
RPRO; IPR001368; -.
HDNVCSGNREATQKCGIDVTLCEEAFFREAVPTKIIPNWLSVLVDSLPGTKVNAESVERI
                                  HRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNAT
                                                         LCVPCPDHSYTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVCECEEGRYLEIEFCLK
||||||||||||SWHTSDECVYCSPVCKELQSVKQECNRTHNRVCECEEGRYLEIEFCLK
                         HRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AB013898; BAA28269
AB013903; BAA33388
AB013899; BAA33388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P25942; 1CDF
                                                                                                                                                                        401
                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BAA33388.
BAA33388.
BAA33388.
                                                                                                                                                                                                                                                                                                                              21
401
201
63
106
143
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365
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62
80
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JOINED.
JOINED.
                                                                                                                                                                                                                                                                                          4 X TNFR-CYS.
TNFR-CYS 2.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 3.
TNFR-CYS 4.
DEATH DOMAIN.
BY SIMILARITY.
                                                                                                                              0;
                                                                                                                                                                                       I -> R
SWISS).
N -> D
SWISS).
S -> A
SWISS).
L -> R
                                                                                                                                                                               L -> R
SWISS)
                                                                                                                                                                                                                                          POTENTIAL.
R -> P (IN
SWISS).
I -> R (IN
                                                                                                                            Score 2179;
Pred. No. 2.5
); Mismatches
                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                 OSTEOPROTEGERIN.
                                                                                                                                                                        CAA6102D3B312470 CRC64;
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                                                                                                                                                                                                                                          STRAINS
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2.5e-165;
es 0;
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                                                                                                                              Indels
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                                                                                                                                                                                                                                               008727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
                                                                                                                                                  PFAM, PF00020; TNFR_G6; 4.

PROSITE; PS00652; TNFR_NGFR_1; PROSITE; PS50050; TNFR_NGFR_2; Glycoprotein; Repeat; Cytokine;
                                                                                                                                                                                                  EMBL; U94330; AAB53707.1;
HSSP; P25942; 1CDF.
                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNFRSF11B OR OPG.
                                                                                                                         DOMAIN
                                                                                                                                            SIGNAL
                                                                                                                                                                                         INTERPRO;
                                                                                                                                                                                                                     SIMILARITY).
-!- SUBCELLULAR LOCATION: 1
-!- SIMILARITY: CONTAINS A
                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-INTESTINE
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N
                                                                                                                                                                                 PFAM; PF00020;
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                                                                                                                                                                                                                                                                                                                                                                                           97262071
                                                                                                                                                                                          IPR001368;
22
23
23
64
107
144
306
65
87
118
87
145
PRELIMINARY;
                                                                                                                                                                                                                      EXTRACELLULAR.
A LA-NGFR/TNFR-TYPE
TNER-CYS 2.
TNER-CYS 3.
TNER-CYS 4.
DEATH DOMAIN.
BY SIMILARITY.
                                                                                                               OSTEOPROTEGERIN.
4 X TNFR-CYS.
TNFR-CYS 1.
                                                                                                                                             e; Signal.
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
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                                                                                                                                                                      UNKNOWN_1
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Best Local
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CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                        000300; 060236;
01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
01-MAY-2000 (TREMBLREL. 13, Last annotation update)
0STEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
(OCIF) (TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B).
TNFRSF11B OR OPG OR OCIF.
                                                                                                                                                                Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S., Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
        Yasuda H., Shima N., Nakagawa N., Mochizuki
Sato Y., Goto M., Yamaguchi K., Kuriyama M.,
Tsuda E., Morinaga T., Higashio K.;
"Identity of osteoclastogenesis inhibitory f
                                                                                                                             Davy E., Bucay N., Renshaw-Gegg Campbell P., Sander S., Van G., Suggs S., Boyle W.J.;
"Osteoprotegerin: a novel secret of bone density.";
                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                           TISSUE-LUNG FIBROBLAST;
MEDLINE: 98151033.
                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                     MEDLINE; 97262071.
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                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                          bone density. ;
11 89:309-319(1997).
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POTENTIAL.
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RT "Cloning and characterization of the gene encoding human

RT "Cloning and characterization of the gene encoding human

RT osteoprotegerin/osteoclastogenesis-inhibitory factor.";

RT EUR. J. Biochem. 254:683-691(1998).

CC -!- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES

CC -!- FUNCTION: MAY REGULATE BONE AND ALLOWING ACCUMULATION OF NEWLY

CC OF OSTEOCLAST DEFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY

CC SYNCHESIZED BONE AND CARRILAGE. MAY INHIBIT IN VITRO

CC SYNCHESIZED BONE AND CARRILAGE. MAY INHIBIT IN VITRO

OSTEOCLASTOGENESIS BY INTEROPTING CELL-TO-CELL SIGNALING BETWEEN

CC STROMAL CELLS AND OSTEOCLAST PROGENITORS.

CC -!- SUBGLIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY

CC SUBCELULIAR LOCATION: EXTRACELLULAR.

CC -!- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN LUNG, HEART,

CC INTERED FOR CHARLEST LEVELS IN LUNG, HEART,

CC ANUMERS OF CHARLE HEMODITION OF THE ORDING NOT DETECTED IN
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CONFLICT
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                                                                1 MNKWICCALLVILDI-IEWTTQETLPPKYLHYDPETGHQLICDKCAPGTYLKQHCTVRRK
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L; AB002146; BAA25910.1; -.
L; AB00882; BAA32076.1; -.
L; AB008821; BAA32076.1; JOINED.
L; U94332; AAB53709.1; -.
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TLCVPCPDHSYTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVCECEEGRYLEIEFCL
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POTENTIAL.
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TNFR-CYS 3.
TNFR-CYS 4.
DEATH DOMAIN.
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Pred.
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PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1
PROSITE; PS50050; TNFR_NGFR_2; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia;
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ryota; Metazoa; Chordata;
alia; Eutheria; Primates;
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                                                                                                      CEEAFFRFAVPTKIIPNWLSVLVDSLPGTKVNAESVERIKRRHSSQEQTFQLLKLWKHQN 261
                                                                                                                                                                                                                                                                                                                                                           CKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNATHDNVCSGNREATQKCGIDVTL 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YCSPVCKELQSVKQECNRTHNRVCECEEGRYLEIEFCLKHRSCPPGSGVVQAGTPERNTV 141
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                         SEQLLKLLSLWRIKNGDQDTLKGLMYALKHLKTSHFPKTVTHSLRKTMRFLHSFTMYRLY 381
                                                                                                                                                                                                                                                                                                                                  CKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTL
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                                                                                                                                                                                                                        CEEAFFRFAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKRQHSSQEQTFQLLKLWKHQN
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SDQILKLLSLWRIKNGDQDTLKGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY
                                                                                                                                                                                                                                                                                                                                                                                                                                              YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTV 120
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1789; DB 4;
Pred. No. 2.1e-134;
5; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Pao 31:680-684(1999)
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Best Local Similarity
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SEQUENCE
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Yu K.Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.

"A newly identified member of tumor necrosis factor superfamily (TR6) suppresses LIGHT-mediated apoptosi J. Biol. Chem. 274:13733-13736(1999).

EMBL; AR104419; AADD3056.1; -.

EMBL; AF134240; AADD29688.1; -.

EMBL; AF134240; AADD29688.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      095407;
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PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1

PROSITE; PS01186; EGF 2; UNKNOWN_1.

PROSITE; PS50050; TNFR_NGFR_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischl
Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin
Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 396:699-703(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
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01-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                 VCKELQSVKQECNRTHNRVCECEEGRYLEIEFCLKHRSCPPGSGVVQAGTPERNTVCKKC
                                                                                                                                                                                                                                                                                                                                                                                                                                   PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PKYLHYDPETGHQLLCDKCAPGTYLKQHCTVRRKTLCVPCPDHSYTDSWHTSDECVYCSP
                                                                                                                                                                                          EEAFFRFAVPTKIIPNWLSVLVDSL 227
                                                                                                                                                                                                                                                                                       PDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNATHDNV---CSGNREATQKCGIDVTLC
                                                                                                                                              ERAVIDEVAFQDISIKRLQRLLQAL
                                                                                                                                                                                                                                         PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C
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99087326.
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Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 424.5; DB 4
Pred. No. 3.2e-26;
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                                                                                                                                              236
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Best Local Similarity
Matches 67; Conserv
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Q62327;
Q1-NOV-1996
Q1-NOV-1996
Q1-MAY-2000
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DECOY RECEPTOR.
Salvelinus fontinalis (Brook trout).
Salvelinus fontinalis (Brook trout).
Salvelinus fontinalis (Brook trout).
Salvelinus fontinalis (Brook trout).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo Eukaryota; Meopterygii; Teleostei; Euteleostei; Actinopterygii; Neopterygii; Teleostei; Salmonidae; Salvelinus
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01-MAY-2000
01-JUN-2000
                                          NON_TER
VARIANT
VARIANT
                                                                           PROSITE;
                                                                                                                                                                                                                                                               01-NOV-1996 (TIEMBLIE1 01, Created)
01-NOV-1996 (TIEMBLIE1 01, Last sequence update)
01-NAY-2000 (TIEMBLIE1 13, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR 2 MRNA (FRAGMENT).
                     VARIANT
VARIANT
                                                                                                                                                               MEDLINE; 95178848.
Powell E.E., Wicker L.
"Allelic variation of
                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A tumor necrosis factor receptor homolog is up-regulated trout (Salvelinus fontinalis) ovary at the completion of a Biol. Reprod. 0:0-0(1999).
                                                                                                  PFAM;
                                                                                                                                                     gene.";
                                                                                                                                                                                                   STRAIN-NOD
                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                       Mus musculus (Mouse).
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PROSITE; PS01186; EGF_2; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bobe J., Goetz F.W.;
                                                                                                           Mamm. Genome 5:726-727(1994).
EMBL; X76401; CAA53981.1; -.
HSSP; P19438; INCF.
INTERPRO; IPRO01368; -.
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                                                                                                                                                                                                                                                                                                                                                                                             FSGETSSKAPCIKHTNCSTFGLLLIQKGNATHDNVCS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                              SVKQECNRTHNRVCECEEGRYL - - EIEFCLKHRSCPPGSGVVQAGTPERNTVCKKCPDGF
                                                                                                                                                                                                                                                                                                                                                                                                                          VVKQECSPSNNCECECKEGYYFNKKYEACIKHKECPPGYGANTTGTPHQDTECVQCQAGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF00020; TNFR_c6; 4.
                                                                          PS00652; TNFR_NGFR_1;
PS50050; TNFR_NGFR_2;
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268
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                                                                                                  TNFR_c6; 4
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Rodentia;
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    Created)
    Last sequence up
    Last annotation

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type 2 tumor necrosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 390.5; DB 13;
Pred. No. 1.6e-23;
""amatches 53;
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                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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            Оынны
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factor receptor
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Matches 70
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Best Local S
Matches 66
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EMBL; Y14620; CAA74969.1; JOINED.
EMBL; Y14621; CAA74969.1; JOINED.
EMBL; Y14622; CAA74969.1; JOINED.
EMBL; Y14623; CAA74969.1; JOINED.
EMBL; Y14623; CAA74969.1; JOINED.
HSSB; P19438; INCF.
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088734;
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PROSITE; PS00652; TNFR_NGFR_1;
PROSITE; PS50050; TNFR_NGFR_2;
SEQUENCE 482 AA; 51106 MW;
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"The Mouse Tumor Necrosis Fa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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  156
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                                              124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WITQETLPPKYL--HYDPETGH------
  SKAPCIKHTNCSTFGLLLIOKGNATHDNVCS 186
                                            RVCACEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTFSDTTS
                                                                                      RVCECEEGRYLEIEF
                                                                                                                                    VKHFCNKTSDTVCADSDTVCADCEASMYTQVWNQFRTCLSCSSSCSTDQVETRACTKQQN
                                                                                                                                                                            LKQHCT-----VRRKTLCVPCPDHSYTDSWHTSDECVYCSPVCKELQSVKQECNRTHN
                                                                                                                                                                                                                        LWVALVFELQL--WATGHTVPAQVVLTPYKPEPGYECQISQEYYDRKAQMCCAKCPPGQY
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                                                                                                                                                                                                                                                                                                            ch 13.9%;
l Similarity 33.2%;
70; Conservative 2
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Metazoa; Chordata; C
Metazoa; Rodentia; ؟
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rosis Factor Receptor Gene:Genomic
the two Transcripts.";
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13,
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Pred. No. 3.1e-
20; Mismatches
                                                                                                                                                                                                                                                                                                            Score 302.5;
Pred. No. 2.7e
22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation updat
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3.
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.le-17;
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                                                                                                                                                                                                                                                                                                                                                                                                                            CRC64;
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mic Structure
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RESULT
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DT Q1-
DT Q1-
DT Q1-
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Matches 91
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075509;
01-NOV-1998
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Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AF068868; AAC34583.1; -.
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SEQUENCE FROM N.A.

Pan G., Bauer J.H., Haridas V., Wang S., Liu D., Ni J.,

Vincenz C., Aggarwal B.B., Dixit V.M.;

"Identification and functional characterization of DR6,

"Identification" "NF receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1
PROSITE; PS50017; DEATH_DOMAIN; 1.
PROSITE; PS50050; TNFR_NGFR_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1998
01-MAY-2000
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INTERPRO; IPRO01368; -.
PFAM; PF00020; TNFR_c6; 4.
PFAM; PF00531; death; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STDVCRPHRICS----ILAIPGNASTDAVCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNATHDN 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVLLDIIEWTTQE-----TLPPKYLHYDPETGHQLLCDKCAPGTYLKQHCTVRRKTLCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLALMESLPGKKIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RPKVLSSIQEGTVP-----DNTSSARGKEDVNKTLPNLQVVNHQQGPHHRH----ILK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIKRRHSSQEQTFQLLKLWKHQN----RDQEMVKKIIQDIDLCESSVQRHLGHSNLTTEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VCGTLPSFSSSTSPSPGTAIFPRPEHMETHEVPSSTYVPKGMN-----STESNSSASV 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CPVGWGVRKKGTETEDVRCKQCARGTFSDVPSSVMKCKAYTDCLSQNLVVIKPGTKETDN 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCPVGTFTRHENGIEKCHDCSQPCPWPMIEKLPCAALTDRECTCPPGMFQSNATCAPHTV 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCPDHSYTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVCECEEGRYLEIEFCLKHRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLLLGFLSTTTAQPEQKASNLIGTYRHVDRATGQVLTCDKCPAGTYVSEHCTNTSLRVCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 29.(
91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   655 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TYEMBLrel. 08, Created)
(TYEMBLrel. 08, Last sequence update)
(TYEMBLrel. 13, Last annotation update)
D DEATH RECEPTOR-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY
                                                                                           Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NFR_NGFR_2;
71844 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.8%;
29.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 301.5; DB 4
Pred. No. 4.7e-16;
0; Mismatches 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48939391C4852A33 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150;
                                                                                                                                                                                                                         update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a novel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
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J35305

ID 035305

RELIMINARY;

AC 035305

PRELIMINARY;

AC 035305

PT 01-JAN-1998 (TIEMBLrel. 05, Created)

DT 01-JAN-1998 (TIEMBLrel. 05, Last sequence update)

DT 01-JAN-2090 (TIEMBLREL. 13, Last annotation update)

DE RECEPTOR ACTIVATOR OF NF-KAPPA-B PRECURSOR (TNF-RELATED ACTIVATION-DE INDUCED CYTOKINE RECEPTOR) (RANK).

GN TMARRSFILA OR HANK.

OS Mus musculus (Mouse).

OC EUKaryota; Netazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
Receptor;
SIGNAL
CHAIN
                                               PFAM; PF00020; TNFR_C6; 3.

PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.

PROSITE; PS01186; EGF_2; UNKNOWN_1.

PROSITE; PS50050; TNFR_NGFR_2; 1.

Receptor; Glycoprotein; Transmembrane; Si
                                                                                                                                                                                                                                                     EMBL; AF019046; AAB
HSSP; P25942; 1CDF.
                                                                                                                                                                                                                                                                                                       -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS RANKL.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL)
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH RE
                                                                                                                                                                                                                                                                                                                                                                                  Nature 390:175-179(1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anderson D.M., Maraskovsky Tometsko M.E., Roux E.R., 7 Galibert L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-LIVER EPITHELIUM; MEDLINE; 98032977.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM; PF00020; TNFR_C6; 4.
PROSITE; PS00652; TNFR_NGFR_1;
PROSITE; PS50050; TNFR_NGFR_2;
SEQUENCE 439 AA; 46090 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytokine 2:231-237(1990).
EMBL; S63368; AAB19824.1; -.
HSSP; P25942; 1CDF.
                                                                                                                                                                             MGD; MGI:1314891; Tnfrsf11a.
INTERPRO; IPR000561; -.
INTERPRO; IPR001368; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Two human TNF receptors have similar extracellular, intracellular, domain sequences.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brockhaus M., Lesslauer W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dembic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                     "A homologue of the TNF receptor and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133 AGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNATHDNVCS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 YDPETGH-----QLICDKCAPGTYLKQHCTVRRKTLCVPCPDHSYTDSWHTSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 YAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGTETSDVVCKPCAPGTESNTTSSTDICRPHQICNVVAI----PGNASMDAVCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ECVYCSPYCKELQSVKQECNRTHNRYCECEEGRYLEI-----EFCLKHRSCPPGSGVVQ 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62;
; Glycoprotein;
1 30
31 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR001368; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                  AAB86810.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                             function.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.7%;
35.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Teepe M.C., DuBose R.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 298;
Pred. No. 5
  POTENTIAL.
RECEPTOR ACTIVATOR OF NF-KAPPA-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEBCBE329CC67FF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pan
                                                                                                                                                                                                                                                                                                                                                                                                                                       its ligand enhance T-cell
                                                  Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4;
5.5e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lahm H.W.,
                                                  Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dougall W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               but
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179
                                                                                                                                                                                                                                                                                                                                                                                                                                       growth
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Ol-NOV-1999 (TIEMBLIEL 12, Created)
Ol-NOV-1999 (TIEMBLIEL 13, Last sequence update)
Ol-NAY-2000 (TIEMBLIEL 13, Last annotation update)
RECEPTOR ACTIVATOR OF NF-KAPPA-B PRECURSOR (TNF-RELATED INDUCED CYTOKINE RECEPTOR) (RANK).
TNERSF11A OR RANK.
HOMO Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom
                                                                                                                                                                                                           Anderson D.M., Maras
Tometsko M.E., Roux
Galibert L.;
                                                                                  "A homologue of the TNF and dendritic-cell funct Nature 390:175-179(197)
                         SUBCELLULAR LOCATION:
TISSUE SPECIFICITY: U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WNWVNDACSSLSGNK--ESSGDRCAGSHSATSSQQEVCEGILL---MTREEKMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PNWLSVLVDSLPGTKVNAESVERIKRRH---SSQEQTFQLLKLWKHQNRDQEMV
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                         FOR A CYTOKINE LIGAND KNOWN ON: TYPE I MEMBRANE PROTEIN (
UBIQUITOUS EXPRESSION WITH
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BY SIMILARITY.
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N (POTENTIAL).
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PS50050; TNFR_NGFR_2;
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BY SIMILARITY.

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Pred. No. 2.6e
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                                                                                                                                                                                                                                                                                                       -CKSSEQLLKLLSLWRIK
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Best Local Similarity
Matches 85; Conserv
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O85308;

O85308;

O1. NOV-1996 (TrEMBLrel. 01, Created)

O1-NOV-1996 (TrEMBLrel. 01, Last sequence update)

O1-MAY-2000 (TrEMBLrel. 13, Last annotation update)

SECRETED RECEPTOR BINDING TUMOR NECROSIS FACTOR (CR
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STRAIN-BRIGHTON RED;
MEDLINE; 83117629.
MEDLINE; 83117629.
Pickup D.J., Bastia D., Stone H.O., Joklik W.K.;
"Sequence of terminal regions of cowpox virus DNA:
repeated and unique sequence elements.";
Proc. Natl. Acad. Sci. U.S.A. 79:7112-7116(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00652; TNFR_NGFR_1; PROSITE; PS50050; TNFR_NGFR_2; SEQUENCE 355 AA; 39008 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cowpox virus contains two copies secreted form of the type II TNF Virology 204:343-356(1994).
EMBL; L08906; AAA60952.1; -.
HSSP; P19438; ITNR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-BRIGHTON RED;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cowpox virus (CPV).
Viruses; dsDNA viru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hu F Q., Pickup D.J.; "Transcription of the terminal loop region of vaccinia virus initiated from the telomere sequences directing DNA resolution virology 181:716-720(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 90177240.
Parsons B.L., Pickup D.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BRIGHTON RED;
MEDLINE; 91196263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 94378510.
Hu F.Q., Smith C.A., Pickup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-BRIGHTON RED;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERPRO; IPRO01368; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Infection.
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   VLVDSLPG-
                                                                           IDVEINLYPVNDTSCTRTTTTGLSESISTSELTITMNHKDCDPVFRN------GYFS
                                                                                                                                                  LLIQKG-NATHDNVC-----SGNREATQKCGIDVTL----CEEAFFRFAVPTKIIPNWLS
                                                                                                                                                                                                                                     SSGCKACVSQTKCGIGYG-VSGHTPTGDVVCSPCGLGTYSHTVSSVDKC-EPVPSNTFNY 178
                                                                                                                                                                                                                                                                                                            ----EFCLKHRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGL
                                                                                                                                                                                                                                                                                                                                                                                       TNTQCTPCASDTFTSRNNHLPACLSCNGRCDSNQVETRSCNTTHNRICDCAPGYYCFLKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLLLLSCIIIINSDITP-----HEPSNGKCKDNEYKRHHLCCLSCPPGTYASRLCDSKTN
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   TKV - - - NAESVERIKRRHSSQEQTFQLLKLWKHQNRDQEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           copies of an early II TNF receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 226; DB 12;
Pred. No. 2.2e-10;
9; Mismatches 141
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2C9EE5C0D42FA4B3 CRC64;
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01-MAY-2000
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01-JUN-1998
01-MAY-2000
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057305;
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057098;
              CRMB
                          01-JUN-1998 (TremBLrel. 01-MAY-2000 (TremBLrel. TUMOR NECROSIS FACTOR R)
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LOPATEV V.N., PAISONS J.M.,
Submitted (JAN-1997) to the
EMBL; U87839; AAB94356.1; -
HSSP; P25942; ICDF
Cowpox virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERPRO; IPRO01368; -.
PFAM; PF00020; INFR_C6; 2.
PROSITE; PS000652; INFR_NGFR_1;
PROSITE; PS50050; INFR_NGFR_2;
SEQUENCE 349 AA; 37978 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Camelpox virus (strain CP-1).
Viruses; dsDNA viruses, no RN
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                                                                                                                                                                                                                                                                                                                                   136
                                                                                                                                                                                 289 NLTTE
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                                                                                                                                                                                                         CTLNFEIKCNNKGSSSKQ----
                                                                                                                                                                                                                                                           ESISTSELTITMNHKDCDPVFREEYFSVLNKV--
                                                                                                                                                                                                                                                                                   EATQKCGIDVTL----CEEAFFR--FAVPTKIIPNWLSVLVDSLPGTKVNAESVERIKR-
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                                                               (TrEMBLrel.
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                                                                                         PRELIMINARY;
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 (CPV).
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                           RECEPTOR II HOMOLOG
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06, Last sequence update)
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06, Last sequence update)
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EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                          -LTKAKNDDGIMPHS--ETVTLAGDCLSSVDIYILYS
                                                                                          PRT;
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.2e-10;
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                                      update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

STRAIN-MUNICH OPV89/5(CAT), MUNICH OPV 91/1(CAT);

STRAIN-MUNICH OPV89/5(CAT), MUNICH OPV 91/1(CAT);

Loparev V.N., Parsons J.M., Esposito J.J.;

Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; U90233; AAB94389.1; -.

EMBL; U90228; AAB94384.1; -.

REMBL; U90228; AAB94384.1; -.

RINTERPRO; IPR001368; -.

RINTERPRO; IPR001368; -.

R PFAM; PF00020; TNFR_NGFR_1; UNKNOWN_2.

R PFAM; PF000520; TNFR_NGFR_2; 1.

SEQUENCE 349 AA; 38063 MW; 424EE08FDEDD04CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               uery Match 10.2%; score 222.5; DB 12; Length 349; pst Local Similarity 25.6%; Pred. No. 4.2e-10; atches 81; Conservative 47; Mismatches 144; Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae; Orthopoxvirus.
277 CESSVQRHLGHSNLTTE 293
| | | | | :: : | | | ::
293 CLSSVDIYILYSNTNTQ 309
                                                                                   239
                                                                                                                                                                                                                                                 121 SSGCKACVSQTKCGIGYG-VSGHTPTGDVVCSPCGLGTYSHTVSSVDKC-EPVPSNTFNY 178
                                                                                                                            220 LSVLVDSLPG-TKVNAESVE-RIKRRHSSQEQTFQLLKLWKHQNRDQEMV-KKIIQDIDL 276
                                                                                                                                                                  179 IDVEINLYPVNDTSCTRTTTTGLSESISTSELTITMNHKDCDPVFRDGYFSVLNKVATSG 238
                                                                                                                                                                                                           172 LLIQKG-NATHDNVC-----SGNREATQKCGIDVTL----CEEAF--FRFAVPTKIIPNW 219
                                                                                                                                                                                                                                                                                        116 ----EFCLKHRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGL 171
                                                                                                                                                                                                                                                                                                                                 9 LLVLLDIIEWTTQETLPPKYLHYDPETG------HQLLCDKCAPGTYLKQHC--TVR 57
                                                                                                                                                                                                                                                                                                                                                                                                                    6 LLLLLSCIIINSDITP-----HEPSNGKCKDNEYRHHHLCCLSCPPGTYASRLCDSKTN 60
                                                                                   FFTGQNRYQNISKVCTLNFEIKCNNKDSSSKQ-----LTKAKNDDAIMPHSETVTLVGD 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
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rch completed: December 27, 2000, 10:52:38 b time: 69 sec

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OM protein - protein search, using sw model Run on: December 27, 2000, 10:51:29; Search time 40.66 Seconds (without alignments) 625.862 Million cell updates/sec GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

Title:
Perfect score:
Sequence:

US-09-389-545-2
2179
1 MNKWLCCALLVLLDIIEWTT.....QKLFLEMIGNQVQSVKISCL 401

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

182106 seqs, 63460219 residues

rched:

182106

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR_65:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

																												70
28 29	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	œ	7	ጥ	σ	4	ω	N	÷	Result No.
151 147.5	152.5	153	160	161.5	161.5	163	165.5	166	167	177	179.5	182	184	197.5	199	215.5	216	217	220	233.5	244	261	270	270	312	312	314	Score
ი ი 	7.0	7.0	7.3	7.4	7.4	7.5	7.6	7.6	7.7	8.1	8.2	8.4	8.4	9.1	9.1	9.9	9.9	10.0	10.1	10.7	11.2	12.0	12.4	12.4	14.3	14.3	14.4	Query
277 324	272	461	455	454	454	271	461	255	255	256	314	335	416	425	427	348	349	349	326	325	435	277	305	289	474	461	459	Length
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I37552 JC2395	148700	GORTT1	GOHUT1	157826	GQMST1	S12783	JC4302	JT0752	I38426	в32393	I37383	A40036	JN0006	A26431	GQHUN	T28623	D72175	D36858	GQVZML	в43692	I54182	A60771	A46476	A46515	B38634	A35356	I48854	A
homo	٥				tumor necrosis	OX40 antigen precu	tumor necrosis	lymphocyte activat	4-1BB - human	T-cell antigen	FAS soluble protei	apoptosis-mediatin		nerve growth	nerve growth	hypothetical	G2R protein	gene G4R protein	T2 protein -	0	5	٢	B cell-associated	B cell-associated	tumor necrosis		gene murine	Description

	45	44	43	42	41	40	39	38	37	36	ω 5	34	ω ω	32	31	30
	120.5	120.5	122	125	126.5	128.5	128.5	128.5	131.5	133	137.5	137.5	139	142.5	142.5	143
٠	წ		5. 6	5.7	ა დ	5. 9	5.9	5.9	6. 0	6.1	σ. ω	6.3	6.4	б .5	6.5	6.6
	2918	250	1372	1680	1548	1790	1252	786	. 260	. 1786	915	899	595	3102	2823	327
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٠,٠	A54105	A49053	T25933	A43434	S34583	MMFFB1	S36016	A48456	A46517	MMHUB1	JC6148	·G02428	A42086	T43291	T23064	A46484
	fibrillin-2 precur	CD27 antigen precu	hypothetical prote	furin (EC 3.4.21.7	serine proteinase	laminin beta-1 cha	oocyst wall protei	oocyst wall protei	CD27 antigen precu	laminin beta-1 cha	subtilisin-like pr	subtilisin-like pr	CD30 antigen precu	laminin alpha chai	hypothetical prote	apoptosis-mediatin

ALIGNMENTS

F;151-188/Domain: NGF receptor repeat homology <ngf> Cuery Match</ngf>	A;Molecule type: mRNA A;Residues: 1-459 <resa 1-459="" 2:="" <resa="" a;cross-references:="" a;residues:="" c:superfamily:="" embl:x76401;="" factor="" homology<="" necrosis="" ngf="" nid:g433830;="" pid:g433831="" pidn:caa53981.1;="" recentor="" repeat="" th="" tumor="" type=""><th>A;Reterence number: 148854; MUID:951/8848 A;Accession: 148854 A;Status: preliminary; translated from GB/EMBL/DDBJ</th><th>Mamm. Genome 5, 726-727, 1994 A; Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.</th><th>C:Accession: I48854 R:Dowell, F.F.; Wicker, L.S.: Peterson, L.B.: Todd, J.A.</th><th><pre>C;Species: Mus musculus (house mouse) C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999</pre></th><th>RESULT 1 148854. gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)</th><th></th></resa>	A;Reterence number: 148854; MUID:951/8848 A;Accession: 148854 A;Status: preliminary; translated from GB/EMBL/DDBJ	Mamm. Genome 5, 726-727, 1994 A; Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.	C:Accession: I48854 R:Dowell, F.F.; Wicker, L.S.: Peterson, L.B.: Todd, J.A.	<pre>C;Species: Mus musculus (house mouse) C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999</pre>	RESULT 1 148854. gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)	
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RESULT A35356 tumor necr N;Alternat C;Species C;Ancessi R;Smith, Science 24 A;Title: I A;Referena	Oy 176 Db 178	Qy 118 Db 122	Qy 63 Db 62	Qy 18 ДЪ 2	Query Match Best Local Matches 6
RESULT 2 A35356 A35356 tumor necrosis factor receptor type 2 precursor - human N;Alternate names: 75K tumor necrosis factor receptor C;Species: Homo sapiens (man) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C;Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094 R;Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, Science 248, 1019-1023, 1990 Science 248, 1019-1023, 1990 A;Title: A receptor for tumor necrosis factor defines an unusual family of cellular a A;Reference number: A35356; MUID:90260639	.76 KGNATHDNYCS 186 : : .78 PGNASTDAVCA 188	18CLKHRSCPPGSGVVQAGTPEENTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQ 175	63 VPCPDHSYTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVCECEEGRYLEIEF 117	18 WTTQETLPPKYLHYDPETGHQLICDKCAPGTYLKQHCTVRRKTLC 62	Cuery Match 14.4%; Score 314; DB 2; Length 459; Best Local Similarity 34.6%; Pred. No. 1.6e-14; Matches 66; Conservative 20; Mismatches 79; Indels 26; Gaps 4;
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A; Nolecule type: mRNA
A; Molecule type: mRNA
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A; Residues: 116-140, 'p',142-195, 'R',197-362, 'T',364-461 <HEL>
A; Residues: 116-140, 'p',142-195, 'NID:g339751; PIDN:AAA63262.1; PID:g339752
R; Cross-references: GB:M35857; NID:g339751; PIDN:AAA63262.1; PID:g339752
R; Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.
R; Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.
B; Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.
B; Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.
B; Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.
B; Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.
B; Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.
B; Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.
B; Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.
B; Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.
B; Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.
B; Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.
B; Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.
B; Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.
B; Loetscher, H.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.
B; Loetscher, H.; Lesslauer, H.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, M.; Brockhaus, M.
B; Loetscher, H.; Lesslauer, H.; Lesslauer, H.; Lesslauer, H.; Lesslauer, M.; Lesslauer, M.; Lesslauer, M.; Lesslauer, M.; Lesslauer, Lesslauer, M.; Lesslauer, M.; Lesslauer, M.; Lesslauer, M.; Lesslauer, M.; Lesslauer, Lesslauer, Lesslauer, M.; Lesslauer, Lesslauer, M.; Lesslauer, M.; Lesslauer, M.; Lesslauer
                                                                F:23-416/Product: tumor necrosis ractor receptor types
F:40-76/Domain: NGF receptor repeat homology <NG2>
F:78-119/Domain: NGF receptor repeat homology <NG2>
F:120-162/Domain: NGF receptor repeat homology <NG3>
F:120-162/Domain: NGF receptor repeat homology <NG3>
F:164-201/Domain: NGF receptor repeat homology <NG4>
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A; Title: Two tumor necrosis
A; Reference number: A35010;
A; Accession: B35010
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A;Title: Complementary DNA cloning of a receptor for tumor new A;Reference number: A36007; MUID:90349572
A;Accession: A36007
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A;Title: Two human TNF receptors have similar extracellular, A;Reference number: A48416; MUID:91370690
A;Accession: A48416
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A;Rosidues: 1-195,'R',197-461 <KOH>
A;Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758
A;Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758
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R;KOhno, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires, Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
A;Title: A second tumor necrosis factor receptor gene product can shed a naturally occur A;Reference number: A36475; MUID:91045991
                                                                                                                                                                                                                                                                                                                                                         A; Note: the list of introns is incomplete
C; Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
C; Reywords: duplication; glycoprotein; receptor; transmembrane protein
E;1-22/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GDB:125914; OMIM:191191
A;Map position: 1p36.2-1p36.2
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A; Residues: 23-40;65-69;136-141;300-306
R; Engelmann, H.; Novick, D.; Wallach, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Introns: 26/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-37 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein A; Residues: 27-31 <ENG>
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e 150, 381-386, 1994
jtle: Cloning, sequencing and partial functional characterization of the 5'
Reference number: I38094; MUID:95121934
Accession: I38094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecule type: mRNA; protein Residues: 23-461 <DEM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene: GDB:TNFR2
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intracellular #status predicted
                                                                                                                                                                                                                                                                                                              tumor necrosis factor receptor type 2 #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL: X80021;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NID:g666044; PIDN:CAA56324.1; PID:g825701
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C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999 (;Date: 30-Jun-1992 #text_change 23-Jul-1999 (;Accession: B38634; A40254; S54816 R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H Proc. Natl. Acad. Sci. U.S.A. 88; 2830-2834, 1991 A;Title: Cloning and expression of cDNAs for two distinct murine tumor necro
A;Cross-references: GB:M60469; NID:g199827; PIDN: R;Goodwin, R.3.; Anderson, D.; Jerzy, R.; Davis, Mol. Cell. Biol. 11, 3020-3026, 1929
A;Title: Molecular cloning and expression of the A;Reference number: A40254; MUID:91246168
A;Accession: A40254
                                                                                                                                                                                            A;Reference number: A38634; MUID:91187885
A;Accession: B38634
                                                                                                                                                                                                                                                                                                                                                        tumor necrosis factor receptor type 2 precursor - mouse C; Species: Mus musculus (house mouse)
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                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-474 <LEW>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTVRRKTLCVPCPDHSYTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVCECEEGRYL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EI-----EFCLKHRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTCRPGWYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALAVGLEL - - WAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.3%;
34.7%;
                                                                                              NID:g199827; PIDN:AAA39752.1; PID:g199828
Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19;
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Pred. No. 2.3e-14;
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                                                 type 1 and type 2 murine receptors
                                                                                                                                                                                                                                             distinct murine tumor necrosis facto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85;
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                                                                                                                                                                                                                                                                                        G.C.; Wong, G.H.W.;
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                                                                                  Matches
                                                                                               Local Similarity
 50 LKQHCTVRRKTLCVPCPDHSYTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVCECEE 109
                            σ
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                            LWVALVFELQL--WATGHTVPAQVVLTPYKPEPGYECQISQEYYDRKAQMCCAKCPPGQY
                                                      LCCALLVLLDIIEWTTQETLPPKYL -- HYDPETGH --
                                                                                  Conservative
                                                                                               14.3%;
                                                                                               Score 312; DB 2;
Pred. No. 2.3e-14;
                                                                                  Mismatches
                                                                                    84;
                                                                                                            Length 474;
                                                                                    Indels
                                                       --QLLCDKCAPGTY 49
                                                                                    28;
                                                                                 Gaps
                             63
                                                                                    5
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F;1-22/Domain: signal sequence #status predicted <SIG>F;23-474/Product: tumor necrosis factor receptor type: F;40-77/Domain: NGF receptor repeat homology <NG1>F;79-120/Domain: NGF receptor repeat homology <NG2>

#status

predicted <MAT>

repeat homology

F;166-203/Domain: NGF receptor repeat homology <NG4>

C; Superfamily: tumor necrosis factor receptor type 2 C; Keywords: cytokine receptor; transmembrane protein

A; Molecule type: DNA A; Residues: 1-22 <KIS> A; Status: preliminary A; Reference number: S54816 A; Accession: S54816

submitted to the EMBL Data Library, May 1995 A;Description: Characterization of the promoter region

0f

the murine

p75-TNF receptor

A;Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828 R;Kissonerghis, M.; Fellowes, R.; Feldmann, M.; Chernajovsky, Y.

A; Molecule type: mRNA A; Residues: 1-474 <GOO>

A;Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044 C;Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat

7.4.

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A;Cross-references: GB:M83312; NID:g1553058
A;Note: sequence extracted from NCBI backbone (NCBIN:75206, A;Note: this translation is not annotated in GenBank entry NC;Comment: For an alternative splice form, see PIR:A46515 (Superfamily: CD27 antigen; NGF receptor repeat homology C;Keywords: alternative splicing; transmembrane protein F;105-144/Domain: NGF receptor repeat homology <NGF>
                                                                                                                                                                                                                     A46476
ACCESSION: A46476
A; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Apate: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 26-May-2000
C; Accession: A46476
R; Torres, R.M.; Clark, E.A.
J. Immunol. 148, 620-626, 1992
A; Title: Differential increase of an alternatively polyadenylated mRNA species A; Reference number: A46476; MUID:92105763
A; Accession: A46476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Cross-references: GB:M83312; NID:g1553058; PIDN:AAB08705.1; A:Experimental source: BALB/C, liver A:Note: sequence extracted from NCBI backbone (NCBIP:120357) C:Comment: For an alternative splice form, see PIR:A46476 C;Superfamily: CD27 antigen; NGF receptor repeat homology C:Keywords: alternative splicing C:Keywords: alternative splicing C:Keywords: alternative splicing
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A46516

B cell-associated surface molecule CD40, short splice form - mouse
B cell-associated surface molecule CD40, short splice form - mouse
C:Species: Nus musculus (house mouse)
C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 26-May-2000
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Irimaldi, J.C.; Torres, R.; Kozak, C.A.;
Immunol. 149, 3921-3926, 1992
A;Title: Genomic structure and chromosomal
A;Reference number: A46515; MUID:93094586
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                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-305 < TOR>
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A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP--NQGLRVKKEGTAESDTVCTCKEGQHCTSKDCEACAQHTPCIPGFGVMEMATETTDT 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPVCKELQSVKQECNRTHNRVCECEEGRYL---EIEFCLKHRSCPPGSGVVQAGTPERNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KYLHYDPETGHQLLCDKCAPGTYLKQHCTVRRKTLCVPCPDHSYTDSWHTSDEC---VYC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTNCSTFGLLLIQKGNATHDNVCS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VKHFCNKTSDTVCADCEASMYTQVWNQFRTCLSCSSSCTTDQVEIRACTKQQNRVCACEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRYLEIEF-----CLKHRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57; Conservative
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Pred. No. 1.1e-11;
6; Mismatches 68
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                                                                                       MUSCD40A, release 113.0
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F;194-215/Domain: transmembrane #status predicted <TMM>
F;216-277/Domain: intracellular #status predicted <CYT>
F;153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmem F;1-20/Domain: signal sequence #status predicted <SIG>F;21-277/Product: B-cell activation protein CD40 #status experimental <MAT>F;21-193/Domain: extracellular #status predicted <EXT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 03-Jun-1993 #sequence_revision 03-Feb-1994
C;Accession: S04460; A60771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein
A; Residues: 21-50 <BRA>
A; Experimental source: B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X60592; NID:g29850; PID:g29851
R;Braesch-Andersen, S.; Paulle, S.; Koho, H.; Nika, H.;
J. Immunol. 142, %62-567, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Title: A B-lymphocyte activation molecule related to the A; Reference number: S04460; MUID:89356608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B-cell activation protein CD40 precursor - human N;Alternate names: B-cell surface antigen Bp50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GDB:215268; OMIM:109535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: GDB:CD40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: A60771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Biochemical characteristics and partial amino acid sequence A; Reference number: A60771; MUID:89093941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-277 <STA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: S04460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Stamenkovic,
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Map position: 20q12-20q13.2
Superfamily: CD27 antigen; NGF receptor repeat homology
136 TGVSDTICEPCPVGFFSNVSSAFEKCHPWTSCETKDLVVQQAGTNKTDVVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 VCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNATHDNVC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 KYLHYDPETGHQLLCDKCAPGTYLKQHCTVRRKTLCVPCPDHSYTDSWHTSDEC---VYC 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                29 LHYDPETG----
                                               TPERNTYCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNATHDNVC 185
                                                                                                                                                                                                              VHPEPPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETECLPCGESEFLDTWNRETHC
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                                                                                                    HQHKYCDPNLG--LRVQQKGTSETDTICTCEEGWHCTSEACESCVLHRSCSPGFGVKQIA
                                                                                                                                        ---VYCSPVCKELQSVKQECNRTHNRVCECEEGRYL---EIEFCLKHRSCPPGSGVVQAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP---NQGLRVKKEGTAESDTVCTCKEGQHCTSKDCEACAQHTPCIPGFGVMEMATETTDT
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                                                                                                                                                                                                                                                                                                                     Similarity 58; Conser
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                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                              12.0%;
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                                                                                                                                                                                                                                                                                                                  Score 261; DB 2;
Pred. No. 4.4e-11;
3; Mismatches 74
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. 1.2e-11;
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                                                                                                                                                                                                                                                                                                                                                                    Length 277;
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186
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A;Status: preiman.
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-325 <UPT>
A;Cross-references: GB.M17433
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
F;64-105/Domain: NGF receptor repeat homology <NG2>
F;64-105/Domain: NGF receptor repeat homology <NG3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Bergh Genomics 16, 214-218, 1993
A;Title: Construction and evaluation of a hncDNA library A;Reference number: 154182; MUID:93252381
A;Accession: 154182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
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A;Map position: 12p13.3-12p13.1
C;Superfamily: tumor necrosis factor receptor type 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession:
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A; Residues: 1-435 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                                          Accession: B43692
pton, C.; DeLange, A.M.; McFadden, G.
plogy 160, 20-30, 1987
prittle: Tumorigenic poxviruses: genomic organization
Reference number: A43692; MUID:87321103
paccession: B43692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein - rabbit fibroma virus
species: rabbit fibroma virus, Shope fibroma virus
pate: 30-Sep_1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
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                    QSVKQECNRTHNRVCECEEGRYLEIE-----FCLKHRSCPPGSGVVQAGTPERNTVCKK 144
                                                                 GHDYEKDGLCCASCHPGFYASRLCGPGSNTVCSPCEDGTFTASTNHAPACVSCRGPCTGH 89
                                                                                                       GHQ-----LICDKCAPGTYLKQHCTVRRKTLCVPCPDHSYTDSWHTSDECVYCSPVCKEL 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VLGLFGLLAASQPQAVPPYASENQTCRDQEKEYYEPQ--HRICCSRCPPGTYVSAKCSRI 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLVLLDIIEWTTQETLPP------KYLHYDPETGHQLLCDKCAPGTYLKQHCTVR 57
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                                                                                                                                                    59;
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54; Conservative
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Conservative
                                                                                                                                                                      10.7%;
31.7%;
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26.9%;
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Pred. No. 1.1e-09;
32; Mismatches 93
                                                                                                                                               Score 233.5; DB 2;
Pred. No. 4.2e-09;
9; Mismatches 91;
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N;Alternate names: B28R protein (COP)
C;Species: variola virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993
C;Accession: D36858; S46888; S32385; S35987
R;Blinov, V.M.
A; Molecule type: DNA
A; Residues; 1-349 < BLI>
A; Residues; 1-349 < BLI>
A; Cross; references: GB: X69198; NID: g456758; PIDN: CAA49137.1; PID: g457087
A; Experimental source: strain India-1967, ssp. major, isolate Ind3
R; Kolykhalov, A.A.; Blinov, V.M.; Gytorov, V.V.; Pozdnyakov, S.G.; Chizh
submitted to the EMBL Data Library, April 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: myxoma virus T2 protein; NGF receptor C;Keywords: glycoprotein C;Keywords: glycoprotein F;64-105_Domain: NGF receptor repeat homology <NG2> F;106-147/Domain: NGF receptor repeat homology <NG3>
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A;Title: Myxoma virus expresses a secreted protein with homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: myxoma virus
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999
C;Accession: A40566
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A; Accession: D36858
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                                                                                                                            A; Status: preliminary
                                                                                                                                                                                            A; Description: not shown
                                                                                                                                                                                                                  submitted to GenBank,
                                                                                                                                                                                                                                                                                                                                            gene G4R protein -
                                                                                                                                                                                                                                                                                                                                                                     D36858
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C;Superfamily: myxoma virus T2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-326 <UPT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Reference number: A40566; MUID:91335768
A;Accession: A40566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 Similarity
53; Conserv
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protein; NGF receptor re
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3.6e-08;
nes 85;
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                            Chizhikov, V.E.;
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A; Description: Nucleotide sequence analysis of the region of variola virus

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A;ACCESSION.
A;Status: preliminary
A;Molecule type: DNA
A;Molecule: 1-349 <SHC>
A;Residues: 1-349 <SHC>
A;Cross-references: GB:Y16780; NID:g5830555; PIDN:CAB54798.1; PID:g5830759
A;Cross-references: Strain Garcia-1966
                                                                                                                                                                                                                                                                                                                                                                      RESULT
D72175
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                                                                                                                                                                          R;Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, submitted to GenBank, March 1998
A;Description: Analysis of the complete coding sequence of DNA of alastrim va A;Reference number: A72150
                                                                                                                                                                                                                                                                         G2R protein - variola minor virus (strain Garcia-1966)
C:Species: variola minor virus
C:Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 20-Jun-2000
C:Accession: D72175
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A:Residues: 31-168 <SHC>
A:Cross-references: EMBL:X69198
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A;Title: Genes of variola and vaccinia viruses necessary
A;Reference number: $32385; MUID:93202281
A;Accession: $32385
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Best Local S
Matches 92
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                                                                                                                                                                                                   the complete coding sequence of DNA of alastrim variola
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A;Experimental source: strain Bangladesh 1975
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: T28623
R;Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, Nature 366, 748-751, 1993
A;Title: Potential virulence determinants in terminal regions c A;Reference number: Z20488; MUID:94088747
A;Accession: T28623
A;Status: preliminary; translated from GB/EMBL/DDBJ
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C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000
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C; Superfamily:
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A; Residues: 1-348 <MAS>
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Best Local
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Best Local Similarity
Matches 92; Conser
                                                                                                                                                                                                                                  Matches
143
                                      136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261 CNNKGSSFKQLTKAKND--DGMMSHSETVTLAGDCLSSVDIYILYSNTNAQDYETDTIS-
                                                                                                                  82
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                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                         YTPPNGKCKDTEYKRHNLCCLSCPPGTYASRLCDSKTNTQCTPCGSGTFTSRNNHLPACL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VPCPDHSYTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVCECEEGRYLEI-----E 116
SVGDVICSPCGFGTYSHTVSSADKCEPVPN-NTFNYIDVEITLYPVNDTSCT----RTTT 197
                                    PERNTYCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQ-KGNATHDNVCSGNREATQK 194
                                                                                                                                                                                             YDPETG------HQLLCDKCAPGTYLKQHCTVRRKTLCVPCPDHSYTDSWHTSDECV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LMYALKHL--KTSHFP-----KTVTHSLRKTMRFL 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGHSNLTTEQLLALMESLPGKKISPEEIERTRKTCKSSEQLLKLLSLWRIKNGDQDTLKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TPCGSGTFTSRNNHLPACLSCNGRCNSNQVETRSCNTTHNRICECSPGYYCLLKGSSGCK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FLSCIIINGRDAAPYT----PPNGKCKDTEYKRHNLCCLSCPPGTYASRLCDSKTNTQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WLCCALLVLLDIIEWTTQETLPPKYLHYDPE-TGHQLLCDKCAPGTYLKQHCTVRRKTLC
                                                                           SCNGRCNSNQVETRSCNTTHNRICECSPGYYCLLKGSSGCKACVSQTKCGIGYG-VSGHT
                                                                                                                  YCSPVCKELQSVKQECNRTHNRVCECEEGRYLEI-----EFCLKHRSCPPGSGVVQAGT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---TITMNHTDCNPVFREEYFSVLNKVATSGFFTGENRYQNISK-----VCTLNFEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SVERIKRRHSS-----QEQTFQLLK-----LWKHQNRDQEMVKKIIQDIDLCESSVQRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLYPVNDTSCT----RTTTTGLSE-------SILTSEL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACVSQTKCGIGYG-VSGHTSVGDVICSPCGFGTYSYTVSSTDKCEPVPN-NTFNYIDVEI 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FCLKHRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQ- 175
                                                                                                                                                                                                                                    87;
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                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                      9.9%;
23.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51;
                                                                                                                                                                                                                                    47;
                                                                                                                                                                                                                                                      Score 215.5; DB 2
Pred. No. 7.9e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 216; DB 7;
Pred. No. 7.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                      156;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                           Length 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of variola smallpox vir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T.R.; Knight, J.C.;
                                                                                                                                                                                                                                    87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84;
                                                                                                                                                                                                                                  Gaps
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                                                                             142
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A; Accession...

A; Molecule type: mRNA
A; Residues: I-427 < JOH>
A; Cross references: GB: MI4764; NID: g189204; rr...
R; Marano, N.; Dietzschold, B.; Earley Jr., J.J.; Schatteman,
A; Cross references and amino terminal sequencing of human melances, and the procession: A60204
A; Reference number: A60204; MUID: 87085574
A; Recession: A60204
A; Molecule type: protein
A; Experimental source: melanoma cell line A875
A; Otte: this sequence has been corrected by a note added in procession: this sequence has been corrected by a note added in procession: Highlan, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.
Arch. Blochem. Blophys. 294, 244-252, 1992
Arch. Blochem. Blophys. 294, 244-252, 1992
Arch. Structural comains of the extracellular domain of huma called in processions.
A;Gene: GDB:NGFR
A;Cross-references: GDB:12023
A;Map position: 17q21-17q22
C;Superfamily: nerve growth f
C;Keywords: duplication; glyc
F;1-28/Domain: signal sequenc
F;29-427/Product: nerve growt
F;29-427/Domain: extracellula
F;32-65/Domain: NGF receptor
F;67-108/Domain: NGF receptor
                                                                                                                                                                                                                                                                            C; Comment: C; Comment: C; Comment: C; Comment: C; Comment: C; Genetics:
                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M21621; NID:g189206; PIDN:AAA36363.1; PID:g189207 C;Comment: This receptor is found on sensory and sympathetic neurons, on C;Comment: The cysteine-rich region of the extracellular domain may form C;Comment: This protein is thought to form a high-affinity receptor when C;Comment: This receptor undergoes both N- and O-linked glycosylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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A; Residues: 183-208 < VIS>
hgal, A.; Patil, N.; Chao, M.
Cell. Biol. 8, 3160-3167, 1988
A; Mitle: A constitutive promoter directs expression of A; Reference number: 157638; MUID:89096903
A; Accession: 157638
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Cell 47, 545-554, 1986
A; Title: Expression and structure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δÃ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-22 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
                         Superfamily: nerve growth factor receptor; NGF receptor Reywords: duplication; glycoprotein; heterodimer; monome; 1-28/Domain: signal sequence #status predicted <SIG>29-427/Product: nerve growth factor receptor #status exp; 29-250/Domain: extracellular #status predicted <EXT>; 22-65/Domain: NGF receptor repeat homology <NG1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rve growth factor receptor precursor, low affinity - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mte: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 22-Jun-1999
ccession: A25218; A60204; S21689; I57638
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ite: 31-Mar-1988 #sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ternate names: NGF receptor
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54, 1986
                                                                                                                                                                                                                           GDB:120234; OMIM:162010
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G.; Thompson,
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LLVLLDIIEWTTQETLPPKYLHYDPETGHQLLCDKCAPGTYLKQHCTVRRKTLCVPCPDH 68

Matches

Similarity

Pred. No. 1.7e-06;

DB 1;

Length

Mismatches

Indels

123;

Gaps

19;

Conservative

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A; Cross-references: GB:X61269 C; Comment: This receptor is found on sensory and sympathetic neurons, on C; Comment: The cysteine-rich region of the extracellular domain may form C; Comment: This protein is thought to form a high-affinity receptor when C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;109-147/Domain: NGF receptor repeat homology <NG3>F;149-189/Domain: NGF receptor repeat homology <NG4>F;197-248/Region: serine/threonine-richF;251-272/Domain: transmembrane #status predicted <TIF;273-427/Domain: intracellular #status predicted <TIF;260/Binding site: carbohvdrate (Asn) (^Ovalont) ***---
                                                                            F;30-425/Product: nerve growth factor receptor *status F;30-251/Domain: extracellular *status predicted <EXT>F;30-65/Domain: NGF receptor repeat homology <NG1>F;68-109/Domain: NGF receptor repeat homology <NG2>F;110-148/Domain: NGF receptor repeat homology <NG3>F;150-190/Domain: NGF receptor repeat homology <NG3>F;150-190/Domain: NGF receptor repeat homology <NG4>F;198-249/Region: serine/threonine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-425 <RAD>
A;Cross-references: GB:X05137; NID:g56755; PIDN:CAA28783.1; PID:g56756
A;Cross-references: GB:X05137; NID:g56755; PIDN:CAA28783.1; PID:g56756
A;M:Timmusk, T.; Allikmets, R.; Saarma, M.; Persson, H.
Gene 121, 247-254, 1992
A;Title: Regulatory elements and transcriptional regulation by testost:
A;Reference number: PH1229; MUID:93077038
A;Accession: PH1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Radexe, m.u., 1987
Nature 325, 593-597, 1987
A;Title: Gene transfer and molecular cloning of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N;Alternate names: NGF receptor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10
C;Accession: A26431; PHI229
R;Radeke, M.J.; Misko, T.P.; Hsu, C.; Her
F;252-273/Domain: transmembrane #status predicted <MEM>F;274-425/Domain: intracellular #status predicted <INT>F;61/Binding site: carbohydrate (Asn) (covalent) #statu
                                                                                                                                                                                                                                                                                         A;Introns: 20/3
C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprote F;1-29/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: A26431;
A; Accession: A26431
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A; Residues: 1-20 <MET>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 LLLLLGVSLGGAKEACPTGLYTHSGE-----CCKACNLGEGVAQPCGA-NQTVCEPCLDS
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31.7%;
(Asn) (covalent) #status
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Pred. No. 1.4e-06;
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C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma C;Comment: The cysteine-rich region of the extracellular domain may form part or all of C;Comment: This protein is thought to form a high-affinity receptor when it associates C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology C;Reywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; F;1-20/Domain: signal sequence #status predicted <SIC>F;21-20/Domain: nerve growth factor receptor #status predicted <MAT>F;21-239/Domain: NGF receptor repeat homology <NG1>F;21-239/Domain: NGF receptor repeat homology <NG2>F;101-139/Domain: NGF receptor repeat homology 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA A;Residues: 21-35,'x','37-172,'K',174-275,'S',277-395,'R',397-416 <HEU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Large, T.H.; Weskamp, G.; Helder, J.C.; Radeke, M.J.; Misko, T.P.; Shooter, E.M.;
Neuron 2, 1123-1134, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nerve growth factor receptor, low affinity precursor - chicken N; Alternate names: NGF receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Experimental source: embryonic chick brain developmental source: embryonic chick brain developmental expression of the chicken NGF receptor.
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Accession: A60504
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Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
    52/Binding site: carbohydrate
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Residues: 1-416 <LAR>
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                                                    transmembrane #status predicted <MEM>
intracellular #status predicted <INT>
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(Asn) (covalent) #status predicted
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Best Local Similarity
153 VDPCLPCTICEE-NEVMVKECTATSDAEC 180
                               157
                                                                                        100 THNRVCECEEGRYLEIEF --- CLKHRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSS 156
                                                               94
                                                                                                                           36
                                                                                                                                             41 CDKCAPGTYLKQHCTVRRKTLCVPCPDH-SYTDSWHTSDECVYCSPVCKELQSVKQECNR 99
                                                                                                                         CKACNIGEGVVQPCGV-NQTVCEPCLDSVTYSDTVSATEPCKPCTQ-CVGLHSMSAPCVE 93
                               KAPCIKHTNCSTFGLLLIQKGNATHDNVC 185
                                                               SDDAVCRCAYG-YFQDELSGSCKECSICEVGFGLMFPCRDSQDTVCEECPEGTFSDEANF 152
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    Conservative

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Pred. No. 1.4e-05;
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Search completed: December 27, Job time: 188 sec 2000, 10:54:37

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Title:
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1 MNKWLCCALLVLLD
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Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Database :

SwissProt_39:*

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Result No.	Score	Query Match	Length	BB	ID	Description
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24		7.0	461	هــو ه	TNR1_RAT	ratt
25	152.	•	272	-	OX40_MOUSE	P47741 mus musculu
26			277	ب.	OX40_HUMAN	Ψ
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33			1680	Н		P30432 drosophile

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Q93038 h wsl-1 pro	P02468 mus musculu	P21849 giardia lam	Q60675 mus musculu	P19137 mus musculu	P31696 gallus gall	Q04592 mus musculu	Q00174 drosophila	P11047 homo sapien	P15215 drosophila	P35556 homo sapien	P41272 mus musculu

ALIGNMENTS

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SEQUENCE OF 22-40; 65-69; 136-141; 300-306 AND 346-362. MEDLINE; 91056048.	***************************************	or necrosis factor receptors.";	 Evidence for immunological cross-reactivity with ce 	crosis factor-binding proteins purific	H . Novick D . Wallach D	SEQUENCE OF A/-SI.		c. Natl. Acad. Sci. U.S.A. 87:6151-	of a shed form of the recep	mentary DNA cloning of a receptor for tumor		.A., Song	90349572.	UENCE	(C) (C) (A) (A)	cite italian There Sene.	in G.M.;	Stallard B.J.,	C.P., White P.S., Maris J.M., Sulman E.P.,	96299745.	SEQUENCE FROM N.A.		naturally occurring tumor necrosis ractor innibitor."; Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335/1990)	mor necrosis ractor receptor gene product	, squires C.H., Enompson K.C., vannice J.L.;	Brewer M.T., Baker S.L., Schwartz P.E	NE; 91045991.	SEQUENCE FROM N.A.		Science 248:1019-1023(1990).	llular and viral proteins.";	"A receptor for tumor necrosis factor defines an unusual family of	D. Goodwin R.G.:	T., Anderson D., Solam L., Beckmann M.P., Jerzv R.	PROM N.A		Eutheria; Primates; Catarrhini	yota; Metazoa; Chordata; Craniata; Ve	Homo sabiens (Human).	B OR THER OR THEBR.	BINDING PROTEIN 2) (TRPII) (P80) (TNF-R2) (P75) (CD120B) (ETANERCEPT).	otation update)	01-AUG-1991 (Rel. 19, Last sequence update)	Created)	33;	TUBAN STANDARD.	RESULT 1

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EMBL;
EMBL;
EMBL;
EMBL;
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Purification and partial amino acid sequence analysis of two distinct tumor necrosis factor receptors from HL60 cells."; J. Biol. Chem. 265:20131-20138(1990).
Phosphorylation;
SIGNAL 1
CHAIN 23
                        PFAM; PF00020; TNFR_C6; 4.

PROSITE; PS00652; TWFR_NGFR_1; 2.

PROSITE; PS50050; TNFR_NGFR_2; 4.

Receptor; Transmembrane; Glycoprotein; Repeat; Phosphorylation; Pharmaceutical; 3D-structure.
                                                                                                                                                PIR;
PIR;
PIR;
PIR;
PIR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Structural basis for human TRAF2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Park Y.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 99221490.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pennica D., Lam V.T., Mize N.K.,
Lipari M.T., Goeddel D.V.;
"Biochemical properties of the 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHARACTERIZATION
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Brockhaus M.;
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                                                                                                     INTERPRO; IPR001368; -.
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PHARMACECUTICAL: AVAILABLE UNDER THE NAME ENBREL (IMMUNEX AND PHARMACECUTICAL: AVAILABLE UNDER THE STREET RESIDUES.

WYESTH -AVERST). USED TO TREAT MODERATE TO SERVERE RHEUMATOID ARTHRITIS (RA). ENBREL CONSIST OF THE EXTRACELLULAR LIGAND-BINDING PORTION OF THERE LINKED TO AN IMMUGLOBULIN FC CHAIN. IT BINDS TO THE ALPHA AND BLOCKS ITS INTERACTIONS WITH RECEPTORS.

SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION. SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION. DATABASE: NAME-PROW; NOTE-CD guide CD120b entry;
WWW-"HTTP://WWW.CDBI.LIM.NIH.GOV/PROW/CD/CD120B.HTM".

DATABASE: NAME-ENDRELINFO.COM/".
                                                                                                                                                            ; A35356; A35356.
; A36007; A36007.
; A36475; A36475.
; B35010; B35010.
                                                                                                                                                                                                                                                                US2158; AAC50622.1; US2159; AAC50622.1; US2160; AAC50622.1; US2161; AAC50622.1; US2162; AAC50622.1; US2162; AAC50622.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNA-ALPHA AND APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW
                                                                                                                                                                                                                        U52163; AAC50622
U52164; AAC50622
M55994; AAA36755
                                                                                                                                                                                                                                                                                                                                          U52156; AAC50622.
U52157; AAC50622.
                                                                                                                                                                                                                                                                                                                                                                      M32315; AAA59929.
M35857; AAA63262.
U52165; AAC50622.
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                                                                                                                                  12-APR-99
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 TUMOR NECROSIS FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Weber R.F.,
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RESULT 2
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Best Local
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                                                                                                                                            Lewis M., Tartaglia L.A., L
Wong G.H., Chen E.Y., Goedd
"Cloning and expression of
necrosis factor receptors d
specific.";
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TRANSMEM
DOMAIN
DOMAIN
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                      TNR2_MOUSE STANDARD; PRT; 474 AA.

P25119; P97893;

01-MAY-1992 (Rel. 22, Created)

01-MAY-1992 (Rel. 22, Last sequence update)

15-JUL-1999 (Rel. 38, Last annotation update)

TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TNF-R2) (P75).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                   TNFRSF1B OR TNFR2 OR TNFR-2.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata
Goodwin R.G., Anderson Copeland N.G., Jenkins
                                               SEQUENCE FROM N.A. MEDLINE; 91246168.
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE; 91187885.
                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                            Chordata;
Rodentia;
                                                                                                                                                                                                                       .A., Lee A.,
Goeddel D.V
     N.A.,
                                                                                                                          U.S.
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4 X TNFR-CYS.
TNER-CYS 1.
TNER-CYS 2.
TNER-CYS 3.
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Pred. No. 1
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BY SIMILA
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Sciurognathi;
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603B580ECD67636F CRC64;
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                                                                                                                                                                                                                                                Bennett G.L., Rice
                           Davis
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1.9e-15;
1es 85;
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                                C.I.
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CARBOHYD
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SIGNAL
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; B38634; B38634.
HSSP; P19438; 1NCF.
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-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-LIVER;
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Mol. Cell. Biol, 11:3020-3026(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAIN
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VKHFCNKTSDTVCADCEASMYTQVWNQFRTCLSCSSSCTTDQVEIRACTKQQNRVCACEA 123
                                                       LKQHCTVRRKTLCVPCPDHSYTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVCECEE 109
                                                                                                                      LWVALVFELQL---WATGHTVPAQVVLTPYKPEPGYECQISQEYYDRKAQMCCAKCPPGQY
                                                                                                                                                                                     LCCALLVLLDIIEWTTQETLPPKYL--HYDPETGH-------QLLCDKCAPGTY 49
                                                                                                                                                                                                                                                                                    Similarity
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PS50050; TNFR_NGFR_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane;
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BY SIM
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                                                                                                                                                                                                                                                                                 Score 312; DB 1;
Pred. No. 2.8e-15;
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                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                   84;
                                                                                                                                                                                                                                                                                                        Length 474;
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RESULT 3
CD40_MOUSE
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EMBL; M94126; AAA37404.1; J
EMBL; M94129; AAA37404.1; J
EMBL; M94128; AAA37404.1; J
EMBL; M94127; AAA37404.1; J
EMBL; M94127; AAA37404.1; J
EMBL; A46476; A46476.
DOMAIN
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DOMAIN
DOMAIN
                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CD40_MOUSE P27512;
                                                                Receptor;
                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE: 93094586.
Grimaldi J.C., Torres R.,
HOward M., Cockayne D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Torres R.M., Clark E.A.;
"Differential increase of an al species of murine CD40 upon B J. Immunol. 148:620-626(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1992 (Rel.
01-OCT-1996 (Rel.
15-JUL-1999 (Rel.
                                                                                                                 PFAM;
                                                                                                                                                                                                                                                                                                                                                       -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases [3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD40L RECEPTOR
                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE; 92105763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNFRSF5 OR CD40.
                                                                                                                                          MGD; MGI:88336; TNFRSF5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Forres R.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REVISIONS
                                                                                                                                NTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                       Genomic structure and chromosomal mapping of the murine CD40 I. Immunol. 149:3921-3926(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GRYLEIEF-----CLKHRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIK
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                                                                                          PS50050;
                                                                                                                              IPR001368;
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                                                                                                           TNFR_c6; 4.
                                                                                                                                                        1CDF
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el. 34, Last sequence update)
el. 38, Last annotation update)
el. 38, Last annotation update)
. PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40).
                                                                                                                                                                                                                                                                                                                                                                                                                                            Torres R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                               TNPR_NGFR_1; 1.
TNFR_NGFR_2; 4.
Glycoprotein; Transmembrane;
19 POTENTIAL.
  289
193
215
289
187
                                                                                                                                                                                JOINED.
JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Kozak C.A., Chang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     n alternatively polyadenylated B lymphocyte activation.";
CD40L RECEPTOR.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
4 X TNFR-CYS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            R., Clark E
                                                                           Repeat;
                                                                                                                                                                                                                                                                                                              restrictions
                                                                           Signal.
                                                                                                                                                                                                                                                                                                                           EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA
                                                                                                                                                                                                                                                                                                                            a collaboration
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Best Local S
Matches 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD40_HUMAN
P25942;
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CARBOHYD
SEQUENCE
             use by modified
                                                                                                                                                            Protein
                                                                                                                                                                                                             Singh J.,
Zheng Z.,
                                                                                                                                                                                                                                                                Proteins [3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TUMO.
TNFRSF5 OR CD4.
Homo sapiens (Human).
Homo sapiens (Human).
Horia; Metazoa; Chordata; Metazoa; Primates;
                                                                  This
                                                                                                                                                                                                                                                                                                MEDLINE; 97189482.
Bajorath J., Aruffo A.;
Bajoratruction and analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMAN
  entities
                                                                                                                                  <del>-</del>
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                                                                                                                                                                                                                                        MEDLINE; 98266353.
                                                                                                                                                                                                                                                                            the ligand binding domain Proteins 27:59-70(1997).
                                                                                                                                                                                                                                                                                                                                                                  Stamenkovic I., Clark E.A., "A B-lymphocyte activation m factor receptor and induced EMBO J. 8:1403-1410(1989).
                                                                                                                                                                                                                                                    3D-STRUCTURE MODELING
                                                                                                                                                                                                                                                                                                                                           3D-STRUCTURE MODELING
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27
                                                                                    FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROPERIN.
TISSUE SPECIFICITY: B-CELLS AFTER TWARRY CARCINOMAS.
SIMILARITY: CONTAINS A LA-NGER/TWIRR-TYPE CYSTEINE-RICH REGION.
DATABASE: NAME-PROW; NOTE-CD guide CD40 entry;
WWWW-"HTTP://WWW.NCBI.NLM.NIH.GOV/PROW/CD/CD40.HTM".
                                        European
          SWISS-PROT entry is copyright. It is produced through a collaboration even the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way field and this statement is not removed. Usage by and for commercial
                                                                                                                                                                    h J., Garber E., van Vlijmen H.

g Z., Naismith J.H., Thomas D.;

role of polar interactions in

its receptor CD40.";

ein Sci. 7:1124-1135(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNATHDNVC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPVCKELQSVKQECNRTHNRVCECEEGRYL---EIEFCLKHRSCPPGSGVVQAGTPERNT 140
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57; Conser
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Last annotation update)
SOR (B-CELL SURFACE ANTIGEN
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n molecule need by cytok
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TNFR-CYS 3.
TNFR-CYS 3.
TNFR-CYS 4.
N-LINKED (GLCNAC. . .) (PO:
N-C791CB6D2FEA574E CRC64;
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Pred. No. 1.5e
26; Mismatches
  agreement
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No. 1.5e-12;
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oved. Usage by and for (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                 to the nerve growth
carcinomas.";
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; Homo.
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DOMAIN
                                                                                                                                                                                                             01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS F
2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prosite; ps00652; TNFR_NGFR_1;
prosite; ps50050; TNFR_NGFR_2;
Receptor; B-cell; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an
"Construction and evaluation of transcribed sequences derived Genomics 16:214-218(1993).
                                                   MEDLINE; 93252381.
Baens M., Chaffanet M.,
                                                                                                                                                        Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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                                                                                    TISSUE=LIVER;
                                                                                                                                           Mammalia;
                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                LTBR OR TNFCR OR TNFRSF3.
                                                                                                                                                                                                                                                                                                                       TNRC_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                               136
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                                                                                                        FROM
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                                                                                                                                           Eutheria;
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                                                                                                                                           Chordata;
Primates;
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                                                     Cassiman J.J.,
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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3; Mismatches
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N-LINKED (GLCNAC. . .) (POTENTIAL).
BC8776EC2C4A5680 CRC64;
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EXTRACELLULAR (
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Catarrhini;
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4.
; Transmembrane;
                n J.J., den Berghe H., Maryn
a hncDNA library of human 1
rom a somatic cell hybrid.";
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                                                                                                                                                             Vertebrata; Euteleostomi;
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Crowe P.D., van Arsdale T.L., Walter B.N., Ware Ehrenfels B., Browning J.L., Din W.S., Goodwin "A lymphotoxin-beta-specific receptor.";

Science 264:707-710(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [2]
FUNCTION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L04270;
HSSP; P25942;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMUNE DEVELOPMENT
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                                                                                                                                                                                                                                                               LLVLLDIIEWTTQETLPP------KYLHYDPETGHQLLCDKCAPGTYLKQHCTVR 57
GLVEAAPGTAQSDTTCKNPLE 215
                                     GLLLIQKGNATHDNVCSGNRE 190
                                                                          WALECTHCELLSDCPPGTEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQ
                                                                                                             --LEIEFCLKHRSCPPGS-GVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTF 169
                                                                                                                                                 RDTVCATCAENSYNEHWNYLTICQLCRP-CDPVMGLEEIAPCTSKRKTQCRCQPGMFCAA 134
                                                                                                                                                                                      RKTLCVPCPDHSYTDSWHTSDECVYCSPVCKELQSVKQ--ECNRTHNRVCECEEGRY--- 112
                                                                                                                                                                                                                           VLGLFGLLAASQPQAVPPYASENQTCRDQEKEYYEPQ--HRICCSRCPPGTYVSAKCSRI 75
                                                                                                                                                                                                                                                                                                                                                                                                435
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BY SIMILARI
                                                                                                                                                                                                                                                                                                  Score 244; DB 1;
Pred. No. 1.8e-10;
2; Mismatches 93;
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TNFR-CYS 1.
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POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TNFR-CY
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                                                                                                                                                                                                                                                                                                                                     Length 435;
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Smith C.P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a collaboration
                                                                                                                                                                                                                                                                                                      22;
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P25943;
P25943;
P15947:
P1992 (Rel. 22, Created)
P1-MAY-1992 (Rel. 22, Last sequence update)
P15-JUL-1999 (Rel. 38, Last annotation update)
P15-JUL-1999 (Rel. 38, East annotation update)
                                                                                                                        CARBOHYD
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             "T2 open reading frame from the Shope fibroma virus encodes a solution of the TNF receptor.";

Biochem. Biophys. Res. Commun. 176:335-342(1991).

-!- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TREACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL REACH CELLULAR TARGET AND THEREBY DEAMPENING.

-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE: 91207415.

Smith C.A., Davis T., Wignall J.M., Din W.S., Farrah T., Upton McFadden G., Goodwin R.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Upton C., F∈lange A.M., McFadden G.;
"Tumorigenic poxviruses: genomic organization and DNA
telomeric region of the Shope fibroma virus genome.";
Virology 160:20-30(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shope fibroma virus (strain Kasza) (SFV).
Viruses; dsDNA viruses, no RNA stage; Po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 873:1103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leporipoxvirus.
  91
                       30
                                            36
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sen the Swiss Institute of Bioinformatics and the EMBL
                       GHDYEKDGLCCASCHPGFYASRLCGPGSNTVCSPCEDGTFTASTNHAPACVSCRGPCTGH 89
                                             GHQ----
  QSVKQECNRTHNRVCECT
                                                                              Similarity
                                                                   Conservative
                                           -LLCDKCAPGTYLKQHCTVRRKTLCVPCPDHSYTDSWHTSDECVYCSPVCKEL
                                                                                                                         AA;
                                                                                                                         35132
                                                                              10.7%;
31.7%;
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TNFR-CYS
TNFR-CYS
N-LINKED
N-LINKED
N-LINKED
N-LINKED
                                                                              Score 233.5; DE Pred. No. 7e-10;
                                                                                                                       Mismatches
 FCLKHRSCPPGSGVVQAGTPERNTVCKK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Poxviridae; Chordopoxvirinae;
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                                                                                                                                                                                                                                                                                                                                                                                                        There are no rest
                                                                                        DB
                                                                                                                                                                                                                                       FACTOR SOLUBLE RECEPTOR.
                                                                 91;
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                                                                  Indels
                                                                                        Length 325;
                                                                                                                                    (POTENTIAL).
(POTENTIAL).
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tent is in no
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CPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNATHDNVCSGNREATQKCGIDVTL---

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15;JUL-1999 (Rel. 33, Last sequence update)
15;JUL-1999 (Rel. 38, Last annotation update)
CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (FRAGMENT).
                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                                                                                                                  EMBL; U57745; AAC48710.1; HSSP; P25942; 1CDF.
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01-NOV-1997 (Rel.
15;JUL-1999 (Rel.
                                                                                                                                                REPEAT
                                                                                                                                                                                                                                                                                                PROSITE; PS00652; TNFR_NGFR_1; PROSITE; PS50050; TNFR_NGFR_2;
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Mammalia; Eutheria;
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Q28203;
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                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                     Receptor;
                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cattle.
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                                                                                                                                                                                                                   MAIN
                                                                                                                                                                                                                                 TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IEDLINE; 97281252.

Hirano A., Brown W.C., Estes D.M.;

Cloning, expression and biological function of the bovine

compologue: role in B-lymphocyte growth and differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149
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 29 LHYDPETG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DCDPVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CPPHTYSDSLSPTERCGTSFNYISVGFNLYPV-NETSCTTTAGHNEVIKTKEFTVTLNYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -CEEAF
                                                                                                                                                                                                                                                                                                                            PF00020;
                             60;
                                      Similarity
                                                                                                                                                                                                                                                                                   B-cell; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90:294-300(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Bovine).
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                           Conservative
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                                                                                                                                                                                                                                                                                                                       TNFR_c6;
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. 35, Last sequence upd
. 38, Last annotation v
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103
-- HQLLCDKCAPGTYLKQHCTVRRKTLCVPCPDHSYTDSWHTSDEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                      10.5%;
                                                                                           29983 MW;
                           21;
                          Score 228; DB
Pred. No. 1.4e
21; Mismatches
                                                                                                                                                             TNFR-CYS
TNFR-CYS
                                                                                                                      N-LINKED
                                                                                                                                                                                                                CYTOPLASMIC
                                                                                                                                                                                                                                                          CD40L RECEPTOR
                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL).
                                                                                                                                                INFR-CYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                             746903F30F95F387 CRC64;
                                                                                                                                                                                                       X TNFR-CYS.
                                                                                                                                                                                                                                                                                   Transmembrane; Repeat; Signal.
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                                                                                                                   (GLCNAC . .)
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                          DB 1; 1
1.4e-09;
hes 89;
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                                                   Length 269;
                          Indels
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Query Match

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RESULT 8
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Вb
                     CARBOHYD
CARBOHYD
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-:- FUNCTION: BINDS TO THE-ALPHA AND BETA. PROBABLY PREVENTS THE TREACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL ANTIVIRAL EFFECTS OF THE CYTOKINE.

-:- SIMILARITY: CONTAINS A LA-NGFR/THER-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR
                                                       REPEAT
REPEAT
                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (Second an email to license@isb-sib.ch).
SEQUENCE
           CARBOHYD
                                            CARBOHYD
                                                                                         REPEAT
                                                                                                                                                                                            PIR; A40566; GQVZML.
HSSP; P19438; 1TNR.
                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                             Upton C., Macen J.L., Schreiber M., McFadden G.; "Myxoma virus expresses a secreted protein with homology to the necrosis factor receptor gene family that contributes to viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE; 91335768.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P29825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VT2_MYXVL
                                                                              REPEAT
                                                                                                    DOMAIN
                                                                                                                 CHAIN
                                                                                                                           SIGNĀL
                                                                                                                                                                       PFAM; PF00020;
                                                                                                                                                                                                                  EMBL; A23729;
                                                                                                                                                                                                                              EMBL; M95181; AAA46632.1;
                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                    virulence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Myxoma virus (strain Lausanne)
                                                                                                                                                                                NTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eporipoxvirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEHRYCNPHIGLRIQS---EGTLHTDTICVCVEGQHCTSHTCESCTPHSLCLPGFGVKQI 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VHSEPATACGEKQYPVNSLCCDLCPPGQKLVNDCTEVSKTECQSCGKGEFLSTWNREKYC
                                                                                                                                                PS00652; TNFR_NGFR_1; PS50050; TNFR_NGFR_2;
                                                                                                                                       Glycoprotein;
                                                                                                                                                                                 IPR001368;
                      17
27
27
27
27
105
148
148
181
181
                                                                                                                                                                                                                   CAA01688.1;
                                                                                                                                                                       TNFR_c6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                      104
147
186
181
205
35208
                                                                                                                                      Repeat;
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WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                        TUMOR NECROSIS
4 X TNFR-CYS.
TNFR-CYS 1.
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TNFR-CYS
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                                            (GLCNAC. .
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Best Local Similarity
Matches 92; Conser
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EMBL; X67117; CAA47540.1; -
PIR; D36858; D36858.
PIR; S35987; S35987.
PIR; S46888; S46888.
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SEQUENCE
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01-FEB-1994 (Rel. 28, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                 protective mechanisms.";
FEBS Lett. 319:80-83(1993).
-!- SIMILARITY: CONTAINS 2 LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN-INDIA-1967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN C22/B28 HOMOLOG.
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                                                                                                                            DOMAIN
                                                                                                                                                   PROSITE;
                                                                                                                                                                                                HSSP;
                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                      Shchelkunov S.N., Blinov V.M., "Genes of variola and vaccinia
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 93202281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Orthopoxvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses; dsDNA
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                                                                                                                                                                                   INTERPRO;
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WICCALLVILDIIEWTTQETLPPKYLHYDPE-TGHQLLCDKCAPGTYLKQHCTVRRKTLC 62
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                                                                                                                                                                                               P19438;
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                                                                                                                                                   PS00652;
PS50050;
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31
67
349
                                  Conservative
                                                                                                                                                             TNFR_c6; 2.
52; TNFR_NGFR_1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    viruses,
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                                                                                                                                                  TNFR_NGFR_2;
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38189
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                                              10.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                            W.
                                  51;
                                                                                                  2 X TNFR-CYS.
TNFR-CYS 1.
TNFR-CYS 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 6.5e-09;
4; Mismatches 85;
                                  Score 217; DB 1;
Pred. No. 1.1e-08;
1; Mismatches 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                         NFR-CYS 1.
NFR-CYS 2.
D45D40B5C6E780EF
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 EMBL; U29173;
EMBL; L38423;
EMBL; U30798;
HSSP; P25942;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNRC_MOUSE
P50284;
01-OCT-1996
                                                                                             the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                       This
                                                                                                                                                                                                                                      "The murine lymphotoxin-beta receptor cDNA: sequence trap and chromosomal mapping."; Genomics 30:312-319(1995).
                                                                                                                                                                                                                                                                                                                                                             Force W.R., Walter B.N., Hession (
Browning J.L., Ware C.F.;
"Mouse lymphotoxin-beta receptor.
and expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation updat
LYMPHOTOXIN-LETA RECEPTOR PRECURSOR.
                                                                   or send an email to license@isb-sib.ch).
                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 96163885.
                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-CVB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIBR OR INFOR.
                                                                                                                                         between
                                                                                                                                                                                                                         -!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA.
                                                                                                                                                                                                                                                                                Honjo T.;
                                                                                                                                                                                                                                                                                            Nakamura T.,
                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                   J. Immunol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          318
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                                                                                                                                                                                SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
                                                                                                                                                                                              SUBCELLULAR LOCATION:
                                                                                                             SWISS-PROT entry is copyright. It is produced through a een the Swiss Institute of Bioinformatics and the EMBI European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is
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                                                                                                                                                                                                              DEVELOPMENT
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; AAA68964.1; -.; AAB00846.1; -.; AAA81334.1; -.; 1CDF.
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                                                                                                                                                                                                                                                                                            Tashiro K., Nazarea M., Nakano
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IOFR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 53; Conserv
                SEQUENCE FROM N.A.
MEDLINE; 87051725.
Johnson D., Lanahan A., Buck C
Bothwell M., Chao M.;
"Expression and structure of t
Cell 47:545-554(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
REPEAT
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
Cell
[2]
                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Euthería; F
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REPEAT
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                                                                                                                                                                                                                           NGFR OR TNFRSF16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERPRO; IPROPEAM; PEOMO20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IQGLVEAAPGTSYSDTICKNPPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TFGLLLIQKGNATHDNVCSGNRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEIE--FCLKHR--SCPPGS-GVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QDTVCKTCPHNSYNEHWNHLSTCQLCRP-CDIVLGFEEVAPCTSDRKAECRCQPGMSCVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RKTLCVPCPDHSYTDSWHTSDECVYCSPVCKELQSVKQ--ECNRTHNRVCECEEGR---Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLVLLDIIEWTTQETLPPKYL--------HYDPETGHQLLCDKCAPGTYLKQHCTVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLGLSGLLVASQPQLVPPYRIENQTCWDQDKEYYEPM--HDVCCSRCPPGEFVFAVCSRS 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transmembrane; Glycoprotein; Repeat; 1 30 POTENTIAL.
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                                                                                                                                                                Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 206; DB
Pred. No. 8.5e
32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190
                                          the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 X TNFR-CYS.
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
                                                                              C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LYMPHOTOXIN-BETA RECEPTOR
                                                                                                                                                              Craniata; Vertebrata;
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ωΝ
                                                                                                                                                                                                                                                               ation update)
RECEPTOR PRECURSOR (NGF RECEPTOR)
                                        human NGF
                                                                            Sehgal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; I
1.5e-08;
les 94;
                                                                              Α.,
                                      receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                            Morgan C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 415;
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                                                                                                                                                              Euteleostomi;
; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
                                                                                Mercer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24;
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LLLLLGVSLGGAKEACPTGLYTHSGE----

LLVLLDIIEWTTQETLPPKYLHYDPETGHQLLCDKCAPGTYLKQHCTVRRKTLCVPCPDH

-CCKACNLGEGVAQPCGA-NQTVCEPCLDS

Indels

16;

Gaps

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Query Match
Best Local S
Matches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor gene.";
Mol. Cell. Biol.
-!- FUNCTION: LOW
                                                                                             DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                            DOMAIN
TRANSMEM
DOMAIN
DOMAIN
                                                                      DOMAIN
CAEBOHYD
                                                                                                                                                                                                                                                           REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between the Swiss Institute of Bioinformat the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NT-3, AND NT-4.

SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE BOND FORMATION.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

FIM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.

SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M14764; AAB59544.1;
EMBL; M21621; AAA36363.1;
PIR; A25218; GQHUN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sehgal A., Patil N., Chao M.;
"A constitutive promoter directs expression of the nerve growth factor
                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00652; TNRR_NGFR.1; 3.
PROSITE; PS50050; TNFR_NGFR.2; 4.
PROSITE; PS50017; DEATH_DOWAIN; 1.
Receptor; Neurogenesis; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                  PFAM; PF00020; TNFR_c6; 4. PFAM; PF00531; death; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 89096903
Sengal A., Patil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-22 FROM N.A. MEDLINE; 89096903.
                                                             SEQUENCE
                                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P07174;
MIM; 162010; .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                         Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERPRO; IPRO00488; INTERPRO; IPRO01368;
  ch 9.1%; s
l similarity 31.7%; P
52; Conservative 25;
                                                             AAA36363.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51. 8:3160-3167(1988).
LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGE, BDNF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1NGR.
                                                             Ą,
                                                         250
250
427
189
165
107
147
147
148
43
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43
148
146
146
146
148
180
180
45188
                                                                                                                                                                                                                                                                                                                                                                           Signal.
                                                              MW;
Score 199; DB
, Pred. No. 2.8e
25; Mismatches
                                                                                 DEATH DOMAIN.
BY SIMILARITY
                                                                                                                                                                                                                                               4 X TNFR-CYS.

TNFR-CYS 1.

TNFR-CYS 2.

TNFR-CYS 3.

TNFR-CYS 4.
                                                             N-LINKED (GLCNAC.
B09FA143FB3D625B
                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                     LOW-AFFINITY
             199; DB 1;
No. 2.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                        Glycoprotein; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                                      NERVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Usage
                         Length 427
                                                              CRC64;
                                                                                                                                                                                                                                                                                                                                                      GROWTH
                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                       FACTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for
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Signal; 3D-structure.

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RESULT 1
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PFAM; PF00020; TNFR_C6; 4.

PFAM; PF00531; death; 1.

PROSITE; PS00652; TNFR_NGFR_1; 3.

PROSITE; PS50010; TNFR_NGFR_2; 4.

PROSITE; PS50017; DEATH_DOMAIN; 1.

Receptor; Neurogenesis; Transmembrane;
                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content modified and this statement is not removed. Usage by ancentitles requires a license agreement (See http://www.isb-corsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Regulatory elements and transcriptional regulation by testosterone and retinoic acid of the rat nerve growth factor receptor promoter."; Gene 121:247-254(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NGFR_RAT STANDARD; PRT; 425 AA. P07174; P07174; O1-APR-1988 (Rel. 07, Created) O1-APR-1988 (Rel. 07, Last sequence update) O1-OCT-2000 (Rel. 40, Last annotation update) LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 97449145.
Liepinsh E., Ilag L.L., Otting G., Ibanez "NMR structure of the death domain of the EMBO J. 16:4999-5005(1997).

-1- FUNCTION: LOW AFFINITY RECEPTOR WHICH
                                                                                                                         EMBL; X05137; CAA28783.1;
EMBL; X61269; -; NOT_ANNO
PIR; A26431; A26431.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Radeke M.J., M:
"Gene transfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 87115859.
                                                                                  INTERPRO; IPR000488; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRUCTURE BY NMR OF 334-418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-22 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 325:593-597(1987).
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GP80-LNGFR) (P75 ICD).
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                                                                                                                                                                                                                                                                                            SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE
                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER
                                                                                                                                                                                                                                                                                                                                                   BOND FORMATION.
                                                                                                                                                                                                                                                                                                                                                                               NT-3, AND NT-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VCEAGSGLVFSCQDKQNTVCEECPDGTYSDEANHVDPCLPCTVC 170
                                                                                                             INGR; 29-JUL-97.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNC
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                                                                                                                       A26431.
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er and
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molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C., Herzenberg
cloning of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                              (See http://www.isb-sib
 Glycoprotein; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                    p75
                                                                                                                                                                                                                                                                                                                                                                                            CAN BIND TO NGF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L.A., Shooter E.I rat nerve growth
                                                                                                                                                                                                                                                                                                         CYSTEINE-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                    neurotrophin receptor.";
                                                                                                                                                                                                                                                                                                                                                               THROUGH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NGF
                                                                                                                                                                                                                                       restrictions
                                                                                                                                                                                                                                                                                                                                                               DISULFIDE
                                                                                                                                                                                                              and
                                                                                                                                                                                                                                                     EMBL
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                                                                                                                                                                                                                                                                                                           REGION
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h factor
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RESULT 13
FASA_BOVIN
ID FASA_BOVIN
AC P51867;
DT 01-OCT-1996
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Best Local Similarity 22.1
Matches 55; Conservative
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SIGNAL 1
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                                                                                                                                                                                                                                                         NSRPVNQTPPPEGEKLHSDSGISVDSQSLHDQQTHTQTASGQALKGDGNLYSSLPLTKRE
                                                                                                                                                                                                                                                                                          MYKKIIQ--
                                                                                                                                                                                                                                                                                                                                                             VDSLPGTKVNAESVERIKRRHSSQE-----
                                                                                                                                                                                                                                                                                                                                                                                           ---RECT; WADAE---CEEIPGRWIPRSTPPEGSDSTAPSTQEPEVPPEQDLVPSTVADM
                                                                                                                                                                                                                                                                                                                                                                                                                 SGNREATQKCGIDVTLCEEAFFRF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                             VGSGLVFSCQDKQNTVCEECPEGTYSDEANHVDPCLPCTVCEDTERQL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VTFSDVVSATEPCKPCTE-CLGLQSMSAPCVEADDAVCRCAYGYYQDEETGHCEACSVCE, 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -SYTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVCECEEGRYLEIE--FCLKHRSCP 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLLILGVSSGGAKETCSTGLYTHSGE-----CCKACNLGEGVAQPCGA-NQTVCEPCLDN
                                                                                                                                                                                          EVEKLLNGDTWRHLAGELGYQPEHIDSFTHEAC - - - - PVRALLASW - - - - GAQDSATLDA
                                                                                                                                                                                                                                                                                                                           VTTVMG-----SSQPVVTRGTTDNLIPVYCSILAAVVVGLVAYIAFKRWNSCKQNKQGA
     (Rel. 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      407
                                                                                                                                                        353
                                    STANDARD;
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                                                                                                                                                                                                                       --ISPEEIER-TRKTCKSSEQLLKLLSLWRIKNGDQD--TLKG
                                                                                                                                                                                                                                                                                        -DIDLCESSVQRHLGHSNLTTEQLLA----LMESLPGKK--
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BY SIM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 197.5; I
Pred. No. 3.5e
59; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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DEATH DOMAIN
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CYTOPLASMIC
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                                      323
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Best Local S
Matches 77
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01-OCT-2000 (Rel. 40, Last annotation update)
FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
(APO-1 ANTIGEN) (CD95).
TNFRSF6 OR APT1 OR FAS.
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                             REPEAT
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00652; TNFR_NGFR_1; 2
PROSITE; PS50050; TNFR_NGFR_2; 2
PROSITE; PS50017; DEATH_DOMAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 1 : 1 : 1
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"Cloning and characterization of the bovine Fas.";
DNA Cell Biol. 15:227-234(1996).
-i- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U34794; AAC48546.1;
HSSP; P25445; 1DDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement ( or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovidae; Bovinae; Bos.
   112
                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                            REPEAT
                                                                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERPRO; IPRO00488; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NTERPRO; IPR001368;
                             93
                                                          53
                                                                                       37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTECUTIC ACTIVATION. ACTIVE CASPASE-8 INTILATES THE SUBSCUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN STIMULATED SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY). SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

SUBCELLULAR LOCATION DEATH DOMAIN INVOLVED IN THE BINDING OF FADD, DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION. SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS
                  VKQECNRTHNRVCECEEGRYLEIEFCLKHRSCPPGS----GVVQAGTPERNTVCKKCPDG 148
VEQNCTRTRNTKCRCKSNFFCNSSPC---EHCNPCTTCEHGIIEKCTPTSNTKCK--
                                                        HQFCCQPCPPGKRKNGDCKRDGDTPECVLCSEGNEYTDKSHHSDKCIRCS-ICDEEHGLE 111
                                                                                      HQLLCDKCAPGTYLKQHCTVRRKT-LCVPCPD-HSYTDSWHTSDECVYCSPVCKELQ--S
                                                                                                                                                                                                                                                                                                                                                                                                                         PF00020; TNFR_c6; 3. PF00531; death; 1.
                                                                                                                     17; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.7%;
nilarity 25.6%;
Conservative 3
                                                                                                                                                                                                                                                                                                                                                               Receptor;
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171
171
189
189
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45
81
125
238
                                                                                                                                                                                               AA;
                                                                                                                                                                                                                                        36445
                                                                                                                                                                                             WW;
                                                                                                                     37;
                                                                                                                                                                                                                      TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
                                                                                                                  Score 190.5; DB Pred. No. 8.1e-07; Mismatches 10
                                                                                                                                                                                                               DEATH DOMAIN
                                                                                                                                                                                             4D88A90E9E1F4892 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ruminantia; Pecora; Bovoidea;
                                                                                                                                  8.1e-07;
                                                                                                                    108;
                                                                                                                                              <u>'</u>:
                                                                                                                    Indels
                                                                                                                                                Length
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                                                                                                                  Gaps
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DOMAIN
TRANSMEM
DOMAIN
DOMAIN
                                                                                                               PROSITE; PS00652; TNFR_NGFR_1; 3. PROSITE; PS50050; TNFR_NGFR_2; 3. PROSITE; PS50017; DEATH_DOMAIN; 1
                                                                                                                                                                 HSSP; P07174; 1NGR.
INTERPRO; IPRO00488; -.
INTERPRO; IPRO01368; -.
PFAM; PF00020; TNFR_C6;
                                                                                                                                                                                                     PIR; JN0006; JN0006.
PIR; A60504; A60504.
HSSP; P07174; 1NGR.
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 21-416 FROM N.A. MEDLINE; 90152140.
                                                                                                                                                                                                                                                                                                                                                                                                               Neuron
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                      "Structure and developmental expression receptor in the chicken central nervous Neuron 2:1123-1134(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus (Chicken).
Gallus gallus (Chicken).
Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NGFR
                                                               CHAIN
                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- PTM: N - AND O-CLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE
-!- SIMILARITY: CONTAINS A LA-NORR/TWFR-TYPE CYSTEINE-RICH REG:
-!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                              "Structure and developmental expression Dev. Biol. 137:287-304(1990).
-:- FUNCTION: LOW AFFINITY RECEPTOR WHICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shooter E.M., Reichardt L.F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archosauria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P18519;
                                                                                        Phosphorylation;
                                                                                                                                                                                                                                          -!- SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                      Heuer J.G., Fatemie-Nainie S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOW-AFFINITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GP80-LNGFR) (P75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      293 E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               318 E 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               258 NVHETAEQKVQLLRNWYQSHGKKNAYCTLTKSLPKALAEKICDIVMKDITNERENANLQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 RRHSSQEQTFQLLKLW--KHQNRD-----QEMVKKIIQDI-DLCESSVQRHLGHSNLTT
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                                                                                                                                                                                                                                                                                                                       NT-3,
                                                                                                                                                                                                                                                                                              BOND FORMATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QKCGIDVTLCEEAFFRFAVPTKIIPNWLSVLVDSLPGTK----VNAESVERIK------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QLNLTDVDL--
                                                                                                                                                      PF00020; TNFR_c6; 4. PF00531; death; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90166579
                                                                                                      Neurogenesis; Transmembrane;
                                                                                                                                                                                                                                                                                                                       AND NT-4
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(Rel. 16, Last sequence update)
(Rel. 40, Last annotation update)
(NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
) (P75 ICD)
 240
240
262
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                         RECEPTOR.
EXTRACELLULAR (POTENTIAL)
POTENTIAL.
 CYTOPLASMIC (POTENTIAL) 4 X THER-CYS.
                                                               LOW-AFFINITY NERVE GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                           Wheeler E.F., Box pression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Radeke M.J., Misko T.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 416 AA.
                                                                                                      Glycoprotein; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                      of the system.
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he chicken NG
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                                                                                                                                                                                                                                                                                                                                                             NGF
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Best Local S
Matches 46
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RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P25445;
01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING (APO-1 ANTIGEN) (CD95 ANTIGEN).
TNFRSF6 OR AFTI OR FAS OR FAS1.
                                                                                                                                                      SEQUENCE |
                                                                                                                                                                                                                              Itoh N., Yonehara S., Ishii Sameshima M., Hase A., Seto "The polypeptide encoded by Fas can mediate apoptosis."; Cell 66:233-243(1991).
                                                                                                   Oehm A., Behrmann I.,
Li-Weber M., Richards
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FASA_HUMAN
                          "Purification and molecular cloning of the APO-1 cell surface antigen, a member of the tumor necrosis factor/nerve growth fi
                                                                             Krammer P.H.;
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 91309137.
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1 Similarity 30.9%;
46; Conservative
                                                                                                                                                        FROM N.A., AND SEQUENCE 92268122.
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BY SIMILARITY

BY SIMI
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the
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
SER/THR-RICH.
DEATH DOMAIN.
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Catarrhini; Hominidae;
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                                                                                                   Pawlita M.,
1 J., Trauth
  identity with
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B.C.,
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                                                                                                   G., Klas C., Ponstingl H.,
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SDECVYCSPVCKELQSVKQE--CNRTHNRVCECEEGRYLEIEFCLKHRSCPPGSGVVQAG 134

EINCTRIQNTKCRCKPNFFCNSTVC---EHCDP

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SSKCRRCR-LCDEGHG

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modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION. ACTIVE CASPASS-8 INSTINATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE T-CELLS, OR BOTH.

1. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

1. DOMAIN. CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD, AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.

1. SIMILARITY: CONTAINS A LA-MGER/TMER-TYPE CYSTEINE-RICH REGION.

1. SIMILARITY: CONTAINS A LA-MGER/TMER-TYPE CYSTEINE-RICH REGION.

1. DATABASE: NAME-PROW; NOTE-CD guide CD95 entry;
WWW-"HTTP://WWW.NCBI.NLM.NIH.GOV/PROW/CD/CD95.HTM".
                                                                                                                                                                                                                                                                                                                                                               INTERPRO; IPR000488; INTERPRO; IPR001368; PFAM; PF00020; TNFR_C6; PFAM; PF00531; death; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Huang B., Eberstadt M., Olejniczak E.T., Meadows R.P., Fesik S.W.; "NMR structure and mutagenesis of the Fas (APO-1/CD95) death domain."; Nature 384:638-641(1996).
                                                                                                                                                                                                                                                                                                                         PROSITE; PS00652; TNFR_NGFR_1; ; PROSITE; PS50050; TNFR_NGFR_2; ; PROSITE; PS50017; DEATH_DOMAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                       MIM; 134637;
                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M67454; AAA63174.1;
EMBL; X63717; CAA45250.1;
PIR; A40036; A40036.
PIR; S24543; S24543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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[3]
STRUCTURE BY NMR
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                                                                                                                                                                                                                                                                                                3D-structure.
                                                                                                                                                                                                                                                                                                             Apoptosis;
42
                          19
                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation. European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADAPTOR MOLECULE FADD RECRUITS
TTVETQNLEGLHHDGQFCHK----PCPPGERKARDCTVNGUEPDCVPCQEGKEYTDKAHF
                          TTQETLPPKYLHYDPETGHQLLCDKCAPGTYLKQHCTVR-RKTLCVPCPD-HSYTDSWHT
                                                                Similarity
                                                                                                                                                                                                                                                                                                              Receptor;
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8
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ADD RECRUITS CASPASE-8 TO THE ACTIVATED
                                                                 .58;
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                                                                                                                       MW.
                                                   Score 182; DB
Pred. No. 3.4e
34; Mismatches
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3 x TNFR-CYS.
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
                                                                                                                                                                                                                                                      POTENTIAL.
FASL RECEPTOR.
EXTRACELLULAR
                                                                                                                    DEATH DOMAIN.

N-LINKED (GLCNAC. . .) (P
N-LINKED (GLCNAC. . .) (P
, 0139942535111410 CRC64;
                                                                                                                                                                                                                                           POTENTIAL
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                                                                .4e-06;
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                                                                                                                                                                                                                              (POTENTIAL)
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                                                      114;
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                                                                                                                                                                                                                                                                                                              Repeat;
                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BINDING OF FADD
                                                                                                                                                                                                                                                                                                              Signal;
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Db	Qy	망	Qy	당	Qy
247 GFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQLHGKKEAYDTLIKDLKKANLC 304	232VNAESVERIKRRHSSQEQTFQLLKLWKHQNRDQEMVKKIQDIDLC 277	198TCRKHRKENQGSHESPTLNPETVAINLSDVDLSKYITTIAGVMTLSQVK 246	178 NATHDNYCSGNREATQKCGIDVTLCEEAFFREAVPTKIIPNWLSVLVDSLPGTK 231	146CTKCEHGIIKECTLTSNTKCKEEGSRSNLGWLCLLLLPIPLIVWVKRKEVQK- 197	135 TPERNTYCKKCPDGFFSGET-SSKAPCIKHTNCSTFGLLL

Search completed: December 27, 2000, 10:55:05 Job time: 207 sec

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Gapop 10.0 , Gapext 0.5
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536.5	665	666.5	709	810	928	933	946	971.5	973	1029	1073	1075.5	1096	1334	1481.5	1486.5	1510	1539	1620	1645	1645		1670.5	~1	1828	1849		1862.5	1875	1879	1880	1882
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W89229	R99929	R99930	R99946	W89228	R99950	Y77464	W89232	W89227	R99945	W89230	W89231	W89226	W89224	R99944	W83928	R99940	R99949	R99941	R99937	R99938	R99939	R99943	R99936	R99357	R99924	R99948	W57636	W53238	R99935	R99933	993	R99942
Tumour necrosis fa	Osteoclastogenesis	stoger	Mutated OCIF, OCIF	_	OCIF,	Primate protein se	Human osteoprotege	Tumour necrosis fa	Mutated OCIF, OCIF	Rat osteoprotegeri	Mouse osteoprotege	Tumour necrosis fa	Tumour necrosis fa	Mutated OCIF, OCIF	THMA-07	, E)	OCIF,	Mutated OCIF, OCIF	•	`	OCIF,	OCIF,	OCIF,	Human tumour necro	Mature osteoclasto	Mutated OCIF, OCIF	2	Human OCIF genome	OCIF,	OCIF,	OCIF,	•

ALIGNMENTS

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W38344
                       03-SEP-1996;
22-DEC-1995;
                                                                                                                                                  CDS
                                                                                                                                                                                                           osteopaenia;
                                                                                                                                                                                                                     antisense oligonucleotide; probe; detection; screening; mouse; bone disease; osteoporosis; Paget's disease; hypercalcaemia; hyperparathyroidism; rheumatoid arthritis; osteomyelitis; osteolytic metastasis; periodontal bone loss; bone necrosis;
                                                                                                                                                                                                                                                                   Osteoprotegerin; antibody; diagnosis; affinity purification; recombinant production; transgenic animal; treatment; prevention;
                                                                                                                                                                                                                                                                                                     Mouse osteoprotegerin
                                                                                                                                                                                                                                                                                                                                                    W38344;
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(AMGE-) AMGEN INC.
                                                        20-DEC-1996;
                                                                               26-JUN-1997.
                                                                                                     DE19654610-A1
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                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                            murine.
                     96US-0706945.
95US-0577788.
                                                        96DE-1054610
                                                                                                                                                  Location/Qualifiers 90..1295
                                                                                                                                      /*tag=
                                                                                                                           /product= osteoprotegerin
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RESULT
W38343
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Rat; osteoprotegerin; antibody; diagnosis; affinity purification;
                                 Rat osteoprotegerin
                                                                    20-APR-1998
                                                                                                                                     W38343 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MNKWLCCALLVLLDIIEWTTQETLPPKYLHYDPETGHQLLCDKCAPGTYLKQHCTVRRKT 60
                                                                                                                                                                                                                                                                                                                                                                           KRRHSSQEQTFQLLKLWKHQNRDQEMVKKIIQDIDLCESSVQRHLGHSNLTTEQLLALME
                                                                                                                                                                                                                                                                                                            SLPGKKISPEEIERTRKTCKSSEQLLKLLSLWRIKNGDQDTLKGLMYALKHLKTSHFPKT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1997-334271/31
DB; T96062.
                                                                                                                                                                                                                      vthslrktmrflhsftmyrlygklflemignqvqsvkiscl
                                                                                                                                                                                                                                                                                       slpgkkispeeiertrktcksseqllkllslwrikngdqdtlkglmyalkhlktshfpkt
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                                                                                                                                                                                                                                                                                                                                                                                                                                          HDNVCSGNREATQKCGIDVTLCEEAFFREAVPTKIIPNWLSVLVDSLPGTKVNAESVERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNAT 180
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                                                                (first entry)
                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 2179; DB 18; 100.0%; Pred. No. 2.1e-179; tive 0; Mismatches 0;
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                                                                                                                                     401
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                        antibodies can be used in OPG diagnostic assays, and as affinity purification materials. The OPG cDNA can be used to express recombinant OPG and to generate transgenic animals. It can also be used to regulate the level of OPG in mammals, specifically to increase OPG levels, however the use of antisense sequences is also contemplated. Fragments of the CDNA can be used as probes to detect OPG expressing cells and tissue, and to screen cDNA libraries for related sequences. OPG can be used to treat or prevent bone diseases, specifically excessive bone loss, e.g. osteopyric metastases, periodontal bone loss, bone necrosis and osteolytic metastases, periodontal bone loss, bone necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antisense oligonucleotide; probe; detection; screening; bone disease; osteoporosis; Paget's disease; hypercalcaemia; hyperparathyroidism; rheumatoid arthritis; osteomyelitis; osteolytic metastasis; periodontal bone loss; bone necrosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diseases involving excessive bone loss, e.g. osteoporosis
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22-DEC-1995;
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                                                                                                                                                             121 HRSCPPGSGYVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNAT
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                                                                                                                                                                                                                                      51
                                                                                                                                                                                                                                                               1 MNKWICCALLVILDIIEWTTQETLPPKYLHYDPETGHQLLCDKCAPGTYLKQHCTVRRKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present sequence is rat osteoprotegerin (OPG).
                                                                                    SLPGKKISPEEIERTRKTCKSSEQLLKLLSLWRIKNGDQDTLKGLMYALKHLKTSHFPKT
                                                                                                                                                                                                                     LCVPCPDHSYTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVCECEEGRYLEIEFCLK 120
                                            KRRHSSQEQTFQLLKLWKHQNRDQEMVKKIIQDIDLCESSVQRHLGHSNLTTEQLLALME 300
                                                                                                                                              hrscppglgvlqagtperntvckrcpdgffsgetsskapcrkhtncsslgllllqkgnat
                             krrhssqeqtfqllklwkhqnrdqemvkkiiqdidlcessvqrhighanltteqlrilme
                                                                                                                                                                                                         lcvpcpdysytdswhtsdecvycspvckelqtvkqecnrthnrvceceegrylelefclk
                                                                                                                                                                                                                                                                                                                            al Similarity
379; Conser
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95US-0577788
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94.5%;
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and as affinity
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RESULT
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                                                                                                                c claimed methods of identifying agonists and antagonists, i.e.

C compounds that bind to the receptors or ligand, and which activate

( agonist) or inhibit activation of (antagonists) TR1, TR3, TR5 or

TI3. A screening kit for identifying agonists, antagonists

TR3, TR5 or

TI3 polypeptides is provided. The agonists and antagonists are

useful for treatment of chronic and acute inflammation, arthritis,

septicaemia, autoimmune disease e.g. inflammatory bowel disease,

psoriasis, transplant rejection, graft versus host disease,

infection, stroke, ischaemia, acute respiratory disease syndrome,

restenosis, brain injury, AIDS, bone diseases, cancer (e.g.

lymphoproliferative disorders), atherosclerosis and Alzheimer's

disease, etc., caused by imbalance of TR1, TR3, TR5 or TL3.
Query Match
Best Local Similarity
Matches 345; Conserv
                                                                                                                                                                                                                                                                                                                                        (TNFR) TR1, also known as osteoprotegerin. The invention relates to TNFR related polypeptides TR1, TR3 and TR5 (see Y05742-44) and their ligand TL3 (see Y05745). TR1, TR3, TR5 and TL3 are used in
                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents tumour necrosis factor receptor (TNFR) TR1, also known as osteoprotegerin. The invention relat
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying agonists and antagonists of tumor necrosis factor related receptors TR1, TR3 and TR5, and of ligand TL3, useful treatment of cancer, AIDS, Alzheimer's disease, bone disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumour necrosis factor receptor; TRI; osteoprotegerin; agonist; antagonist; screening; human; cancer; AIDS; Alzheimer's disease inflammation; arthritis; septicaemia; autoimmune disease; psoriasis; inflammatory bowel disease; transplant rejection;
                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McDonnell PC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-APR-1999
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acute respiratory disease syndrome; restenosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          necrosis factor receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                              Page 10-12;
       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       atherosclerosis; therapy
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                     87.2%;
85.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                              23pp; English.
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       26;
     Score 1900; DB 20; Pred. No. 2.1e-155; 6; Mismatches 29;
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13-AUG-1997;
26-AUG-1997;
                                                                                                                                                                                                                              Tumour necrosis factor receptor; TNF-R; TR1; TR2; TL2; TL4; inflammation; septicemia; autoimmune disease; transplant re graft vs. host disease; infection; stroke; ischemia; brain acute respiratory disease syndrome;, restenosis, bone disea
                                                                                                                                                                                                                       athersclerosis;
                                                                                                Brigham-burke MR,
                                                                                                                                                            04-JUN-1998;
                                                                                                                                                                                         EP897114-A2.
                                                                                                                                                                                                        Unidentified
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                                                                                                               (SMIK ) SMITHKLINE BEECHAM CORP
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                                                                                                                                                                                                                                                                     necrosis
                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                             97US-0057550.
97US-0055513.
97US-0056980.
                                                                                                                                                            98EP-0304424
                                                                                                                                                                                                                       Alzheimer's
                                                                                                                                                                                                                                                                    factor receptor (TNF-R)
                                                                                                                                                                                                                                                                                                                 protein;
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                                                                                                                                                                                                                                                                   related polypeptide
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in injury; AIDS;
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necrosis factor receptor (TNF-R) related polypeptides (TR1 and TL4). The method comprises: (a) (i) contacting TR1 or candidate compound in the presence of TL2 or TL4; or (ii) or

with

TL2 TL2

The invention relates to identifying agonists or antagonists to tumour

Disclosure; Page 11-12;

18pp;

English.

Identifying agonists and antagonists to tumour necrosis receptor (TNF-R) related polypeptides (TRI, TR2, TL2 and useful for treating*stroke, Alzheimer's disease and AIDS

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W83926 w83926 standard;
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                                                                                                                                                                                                                                                                                                                   Human FTHMA-070 protein.
                                                                                                                                                                                                                                                                                                                                                            01-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                    W83926;
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                                                                                                                                                                                                                                                                              FTHMA-070; human; neurological disorder; therapy; diagnosis
17-APR-1998;
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                                                                              WO9848051-A2
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22..401
/label= Mat_protein
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Pred. No. 2.1e-155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated human FTHMA-070 and T85 proteins - used products for the diagnosis and therapy of disorders cellular processes, e.g. neuronal development.
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18-APR-1997;
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                                                       khrscppgfgvvqagtperntvckicpdgffsnetsskapcrkhtncsvfgllltqkgna
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                                                                                 ESLPGKKISPEEIERTRKTCKSSEQLLKLLSLWRIKNGDQDTLKGLMYALKHLKTSHFPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fig 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            401 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid sequence of human FTHMA-070, a novel
                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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97US-0044746.
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                                                                                                                                                                                                                                                                                                                                                                                                                  87.2%;
85.8%;
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Pred. No. 2.1e-155;
6; Mismatches 29;
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Full length osteoclastogenesis inhibitory factor

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                                                                                                                                                                                                                                                                                                                           This sequence represents the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. The OCIF has a molecular weight by SDS-PACE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1996-402320/40
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                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                    osteoporosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1995;
20-FEB-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           encoding osteoclastogenesis inhibitory factor protein - bone resorption control, esp. treatment of osteoporosis
                                           IKRRHSSQEQTFQLLKLWKHQNRDQEMVKKIIQDIDLCESSVQRHLGHSNLTTEQLLALM 299
                                                                                                        KHRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNA 179
                                                                                                                                                                                    khrscppgfgvvqagtperntvckrcpdgffsnetsskapcrkhtncsvfgllltqkgna 17.9
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ikrqhssqeqtfqllklwkhqnkdqdivkkiiqdidlcensvqrhighanltfeqlrslm 299
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N, Shima
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22..401
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Tsuda E, Ue
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Pred. No. 5.6e
26; Mismatches
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Yasuda H;
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                          specifically claimed in the present invention. The present invention describes: (1) a method of inhibiting the formation of osteoclasts and/or antipyretic proteins, which have the following characteristics: (1) MW determined by SDS-PAGE of approximately 60 kDa under reducing conditions, and 60 kDa and 120 kDa under non-reducing conditions; (ii) 401 as sequence (III) (see W53239); (iii), affinity to cation exchangers and heparin; (iv) its osteoclast formation inhibiting activity reduced by heating at 70 degrees Celsius for 10 minutes or 56 degrees Celsius for 30 minutes, and (v) its antipyretic activity reduced by heating at 90 degrees Celsius for 10 minutes, and (2) a method for preparing the above proteins. The proteins are useful for, e.g. treatment and prevention of osteoporosis, rheumatism or multiple sclerosis, and also as antigens for immunological diagnosis of these diseases and disorders.
                                                                                                                                                                                                                                                                                     Inhibition of osteoclast formation and/or antipyretic activity useful for, e.g. treating osteoporosis, rheumatism and multiple sclerosis % \left( 1\right) =\left\{ 1\right\} 
                                                                                                                                                                                                                                                         Claim 4; Page 26-28; 36pp; English.
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W53239 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                         (SNOW ) SNOW BRAND MILK PROD CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9807840-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
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DB; V20768.
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22..401
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Best Local Similarity Matches 344; Query Match

Conservative

;; 50 ;;;

Mismatches

87.0%; 85.6%;

Score 1895; Pred. No. 5

.6e-155; DB 19;

Length 401; Indels

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Gaps

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The present sequence is human osteoprotegerin (OPG). Anti-OPG antibodies can be used in OPG diagnostic assays, and as affinity purification materials. The OPG cDNA can be used to express
                                                                                                                                                                                                                                                                                                                                                                                                    03-SEP-1996;
22-DEC-1995;
                                                                                                   Claim
                                                                                                                                                 Nucleic acid encoding osteoprotegerin - useful for treatment diseases involving excessive bone loss, e.g. osteoporosis
                                                                                                                                                                                                                                                                                                     Boyle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DE19654610-A1
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                                                                                                                                                                                                                                                     WPI;
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95US-0577788
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                                                                                                                                                                                                                                                                                                  Osteoprotegrin; OPG; human; cardiovascular disease; occlusion; calcification; blood vessel; atherosclerosis; medial calcific Monckeberg's arteriosclerosis; therapy.
                                                    23-APR-1998;
                                                                                                      21-APR-1999;
                                                                                                                                                       28-OCT-1999
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Best Local
TR1 receptor; tumour necrosis factor receptor-1; TNF-alpha; TNF-beta; inhibitor; tumour growth; tumour necrosis; microorganism infection; cellular differentiation stimulation; ionising radiation; septic shock; anti-viral response; growth regulator; immune response; meningococcemia; autoimmune disease; apoptosis; inflammation; cachexia; cerebral malaria; AIDS; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     relates to a method of treating or preventing cardiovascular disease by administering OPG. The method can be used to treat and prevent cardiovascular diseases associated with occlusion and calcification of blood vessels, especially atherosclerosis or Monckeberg's arteriosclerosis, i.e. medial calcific sclerosis. Using OPG to treat or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prevent cardiovascular diseases provides an alternative to invasive treatments. OPG can be used as a single therapeutic for prevention and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treating and preventing cardiovascular diseases, especially atherosclerosis and Monckeberg's arteriosclerosis
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                                                                                                    TR1 receptor
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                                                                                                                                                                                        W57635 standard;
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                                                                                                                                                                                                                                                             MNKWLCCALLVLLDI-IEWTTQETLPPKYLHYDPETGHQLLCDKCAPGTYLKQHCTVRRK 59
                                                                                                                                                                                                                                                                                                                     eslpgkkvgaediektikackpsdqilkilslwrikngdqdtlkglmhalkhsktyhfpk
                                                                                                                                                                                                                                                                                                                                       ESLPGKKISPEEIERTRKTCKSSEQLLKLLSLWRIKNGDQDTLKGLMYALKHLKTSHFPK 359
                                                                                                                                                                                                                                                                                                                                                                                             IKRRHSSQEQTFQLLKLWKHQNRDQEMVKKIIQDIDLCESSVQRHLGHSNLTTEQLLALM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mnkllcca-lvfldisikwttgetfppkylhydeetshqllcdkcppgtylkqhctakwk
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                                                                                                                                                                                                                                                                                                                                                                             ikrqhssqeqtfqllklwkhqnkaqdivkkiiqdidlcensvqrhighanltfeqlrslm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLCVPCPDHSYTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVCECEEGRYLEIEFCL 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 37-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of both osteoporosis and cardiovascular diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  401 AA;
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Pred. No. 1e-154;
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                                                                                                                                                                                                                                                                                                                                                                               This sequence is a tumour necrosis factor receptor-1 (TR1) receptor CC of the invention. The DNA can be used to produce a recombinant host CC cell by inserting it into a vector, which is then used to transfect the CC host cell. The TR1 receptor can bind both TNF-alpha and TNK-beta. TR1 CC receptor agonists can be used for inhibition of tumour growth and CC necrosis of tumours. They can also be used to stimulate cellular CC differentiation, e.g. T cell, fibroblasts or haematopoietic cell CC differentiation, may be used to augment TR1's role in the host's defence CC against microorganisms and prevent related disease. The agonists may CC also be used to protect against the deleterious effects of ionising CC radiation produced during a course of radiotherapy, e.g. denaturation of CC enzymes, lipid peroxidation or DNA damage. The agonists may further be used to mediate an anti-viral response, to regulate growth, to mediate the immune diseases and to treat immunodeficiencies related to diseases CS such as HIV. Antagonists to the TR1 receptor may be used to treat autoimmune diseases, e.g. graft versus host rejection and allograft crejection, and T cell mediated autoimmune diseases. They may also be used to treat septic shock, meningococcemia, inflammation, bacterial infections, cachexia, cerebral malaria or AIDS. The products can also be used to read for diseases.
                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated tumour necrosis factor receptor - useful for developi products for treating, e.g. tumours, auto-immune disease(s), graft rejection, apoptosis or inflammation
                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                    1 MNKWLCCALLVLLDI-IEWTTQETLPPKYLHYDPETGHQLLCDKCAPGTYLKQHCTVRRK
\verb|khrscppgfgvvqagtperntvckrcpdgffsnetsskapcrkhtncsvfgllltqkgna|\\
                                                                                       KHRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNA
                                                                                                                                           tvcapcpdhyytdswhtsdeclycspvckelqyvkqecnrthnrvceckegryleiefcl 119
                                                                                                                                                                               TICVPCPDHSYTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVCECEEGRYLEIEFCL 119
                                                                                                                                                                                                                 mnkllcca-lvfldisikwttqetfppkylhydeetshqllcdkcppgtylkqhctakwk
                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                               diagnosing the above diseases
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                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                       27;
                                                                                                                                                                                                                                                                                                      Score 1891; DB 19; Pred. No. 1.2e-154;
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Best Local Similarity
Matches 343; Conserv
                                                                                     This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-C20s in which the 20th Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                          Sequence
                                                                                osteoporosis.
                                                                                                                                                                                                                            Claim 32;
                                                                                                                                                                                                                                               DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis
                                                                                                                                                                                                                                                                                      WPI; 1996-402320/40
N-PSDB; T33162.
                                                                                                                                                                                                                                                                                                                       Goto M, Higashio K,
Nakagawa N, Shima N,
                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1995;
20-FEB-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           osteoporosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mutated OCIF,
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                                                          401 AA;
 Conservative
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95JP-0054977.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Signal peptide"
22..401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers 1..21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label- c20s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note- "Mature OCIF-C20S"
           85.3%;
                                                                                                                                                                                                                        183pp; Japanese.
                                                                                                                                                                                                                                                                                                                      Kobayashi F, Mochizuki
Tsuda E, Ueda M, Yano
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 26;
Score 1885; DB 17;
Pred. No. 4.1e-154;
26; Mismatches 31;
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Claim 29; Page 94-96; 183pp; Japanese
                                            DNA encoding osteoclastogenesis inhibitory factor protein for bone resorption control, esp. treatment of osteoporosi
                                                                                                                                                                                Goto M, Higashio
Nakagawa N, Shima
                                                                                                                                                                                                                                                                                                 21-JUL-1995;
20-FEB-1995;
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                                                                                                                                                                                                                                                  (SNOW ) SNOW BRAND MILK PROD CO LTD.
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                                                                                                              1996-402320/40.
DB; T33161.
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95JP-0054977.
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195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Signal peptide"
22..401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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Tsuda E, Ueda
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da M, Yano
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                                               osteoporosis
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Yasuda H;
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29-AUG-1996
                                                                                                                                                                                                                                                                                                                              Osteoclastogenesis inhibitory
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22..399
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Pred. No. 4.1e-154;
6; Mismatches 31;
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                                 R99934 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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20-FEB-1995;
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                                                                                                    TVTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKIS
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                                                                                                                                 ESLPGKKISPEEIERTRKTCKSSEQLLKLLSLWRIKNGDQDTLKGLMYALKHLKTSHFPK
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u N, Shima
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Tsuda E,
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                                                                                                                                                                                                                                                                                                                                                                                                            Score 1882; DB 17;
Pred. No. 7.3e-154;
6; Mismatches 30;
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R99934;

Mutated 22-APR-1997

OCIF,

OCIF-C22S

(first entry)

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Best Local :
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                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goto M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1995;
20-FEB-1995;
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                                                                                                                                                    KHRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNA 179
                                                                                                  al Similarity 85.1
342; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 100-102; 183pp; Japanese
                                                                                                                                                                                                                                                                       401 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shima
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95JP-0054977
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85.1%;
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Tsuda E, Ueda
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Pred. No. 1.1e-153;
6; Mismatches. 32;
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Yasuda H;
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                                   This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-C21S in which the 21st Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                       {\tt DNA} encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis
                           osteoporosis.
                                                                                                                                                                                             Claim 35; Page 98-100; 183pp; Japanese.
                                                                                                                                                                                                                                                                                                         Nakagawa
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20-FEB-1995;
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DB; T33163.
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N, Shima
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95JP-0054977.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Mature OCIF-C21S"
277
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Tsuda E, l
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Ueda
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eda M, Yano
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Yasuda H;
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                                      120 KHRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNA 179
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84.8%; Pred. No. 1.3e-153;
tive 28; Mismatches 31;
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4.5 Compugen Ltd. S

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Result
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          Score
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US-08-996-139-1

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Best Local Similarity
Matches 401; Conserv

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Score 2179; DB 3; Pred. No. 8.6e-196;); Mismatches 0;

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ALIGNMENTS	US-08-089-458B-6	PCT-US96-03965-2	US-08-236-918A-6	US-08-974-022-52	PCT-US95-17083-4	US-08-152-443A-19	US-08-444-231-19	PCT-US95-17083-2	US-08-409-338-1	US-08-219-237B-2	US-08-974-022-42	US-08-219-237B-6	US-08-232-087A-11	US-08-974-022-50	PCT-US96-12374-2	PCT-US91-02207-4	US-08-292-549-4
	Sequence 6, Appli	Sequence 2, Appli	Sequence 6, Appli	Sequence 52, Appl	Sequence 4, Appli	Sequence 19, Appl	Sequence 19, Appl	Sequence 2, Appli	Sequence 1, Appli	Sequence 2, Appli	Sequence 42, Appl	Sequence 6, Appli	Sequence 11, Appl	Sequence 50, Appl	Sequence 2, Appli	Sequence 4, Appli	Sequence 4, Appli

; LENGTH: 401 amino ac; TYPE: amino acid; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-974-022-4 US-08-974-022-4 Sequence 4, Application US/08974022 Patent No. 6015938 STATE: California COUNTRY: 1.SA COUNTRY: 1.SA ZIP: 91320-1789 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, VG CURRENT APPLICATION DATA: GENERAL INFORMATION: APPLICANT: Boyle, Willaim J. APPLICANT: Lacey, David L. APPLICANT: Calzone, Frank J. APPLICANT: Chang, Ming-Shi TITLE OF INVENTION: OSTEOPROTEGERIN NUMBER OF SEQUENCES: 53 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: ATTORNEY/AGENT INFORMATION: NAME: Winter, Robert B. REFERENCE/DOCKET NUMBER: APPLICATION NUMBER: US/01 FILING DATE: 12-DEC-1995 CLASSIFICATION: PRIOR APPLICATION DATA: CORRESPONDENCE ADDRESS APPLICATION NUMBER: FILING DATE: ADDRESSEE: Amgen Inc. STREET: 1840 Dehavilland Drive CITY: Thousand Oaks STATE: California amino acids US/08/974,022 08/577,788 4: A-378 Version #1.30

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                                                              Matches
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
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APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPRO:
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                                                                                                                                                                                        TYPE: amino acids
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1840 Dehavilland Drive
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Pred. No. 1.9e-186;
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                                                                          NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: OSTEOPROTEGERIN NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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TOPOLOGY:
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STREET: 1840 Dehavilland
CITY: Thousand Oaks
STATE: California
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                                           amino acid
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Lacey, David L.
Calzone, Frank J.
Chang, Ming-Shi
                                                            401 amino acids
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Query Match Best Local (Matches 34)

Local Similarity

85.6%;

Score 1892; DI Pred. No. 5.8e 26; Mismatches

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Length 401; Indels

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Conservative

1 MNKWLCCALLVLLDI-IEWTTQETLPPKYLHYDPETGHQLLCDKCAPGTYLKQHCTVRRK 59

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TLCVPCPDHSYTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVCECEEGRYLEIEFCL 119 MNKLLCCA-LVFLDISIKWTTQETFPFKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWK

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Sequence 2, App....
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                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/794,796
FILING DATE: 04-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Trunch, Alem
APPLICANT: Young, Peter
TITLE OF INVENTION: Tumor Necrosis Related Receptor,
TITLE OF INVENTION: TR4
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 300 amino acid
                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5219 TELEFAX: 610-270-4026
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240 IKRQHSSQEQTFQLLKLWKHQNKAQDIVKKIIQDIDLCENSVQRHIGHANLTFEQLRSLM 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 KHRSCPPGFGVVQAGTPERNTVCKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 KHRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNA 179
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                                                                                                                                                                                        REGISTRATION NUMBER: 34 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: King of Prussia
STATE: PA
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              STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19406
                                                                                                                                                                                                                          Han, William T
                                  amino acid
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                                                  300 amino acids
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linear
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Conservative

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                                                                          ; MOLECULE TYPE: US-08-974-022-41
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Best Local Sim Marity
              Query Match
Best Local
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                                                                                                                                                                                REFERENCE; DOCKET NUMBER: INFORMATION FOR SEQ ID NO: '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                      TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: lina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION: NAME: Winter, Robert B.
                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212 ERAVIDEVAFQDISIKRLQRLLQAL 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203 EEAFFRFÄVPTKIIPNWLSVLVDSL 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Thousand Oaks
                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86 VCKELQSVKQECNRTHNRVCECEEGRYLEIEFCLKHRSCPPGSGVVQAGTPERNTVCKKC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 PKYLHYDPETGHQLLCDKCAPGTYLKQHCTVRRKTLCVPCPDHSYTDSWHTSDECVYCSP 85
                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C
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                 Similarity
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1840 Dehavilland Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Calzone, Frank J.
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              17.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.5%; Score 424.5; DB 39.0%; Pred. No. 6e-32;
                                                                                                                                                                                                                                                                                                                    US/08/974,022
                                                                                                                                                                                                                                                          08/577,788
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                                                                                                                                                                                                 N-378
Score 382; DB 3;
Pred. No. 7.3e-29;
1; Mismatches 3
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88
                            Length 70;
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US-08-974-022-48
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                                                                                                                                                                                                                                                                                      est Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 12-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
187 VVAI----PGNASRDAVCT 201
                              168 TFGLLLIQKGNATHDNVCS 186
                                                                 127 ALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICN 186
                                                                                                                                67 CTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTCRPGWYC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ITLE OF INVENTION: OSTEOPROTEGERIN
                                                                                                                                                                  54 CTVRRKTLCVPCPDHSYTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVCECEEGRYL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Low --
CITY: Thousand Oaks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 YSYTDSWHTS 70
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                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                     9
                                                                                                                                                                                                                                   8 ALLVLLDIIEWTTQETLPPK--YLHYDPETGH------QLLCDKCAPGTYLKQH 53
                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH: 227 amino acids
                                                                                      EI-----EFCLKHRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCS 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALAVGLEL - - WAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVF 66
                                                                                                                                                                                                                                                                          69;
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Chang, Ming-Shi
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Lacey, David L.
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                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                      14.4%; Score 314; DB 3; I 34.7%; Pred. No. 8.7e-22; tive 19; Mismatches 85;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08/577,788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48:
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                                                                                                                                                                                                                                                                                                        Length 227;
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                                                                                                                                                                                                                                                                        26;
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RESULT

APPLICANT:
APPLICANT:

Smith, Craig A. Goodwin, Raymond G. Beckmann, M. Patricia

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                                               RESULT 8
US-08-650-000-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 461 amin -
              Sequence 2, Applic
Patent No. 5945397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence 2, Application US/08385229
Patent No. 5605690
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                         Matches
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wight, Christopher L.
REGISTRATION NUMBER: 31,680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Jacobs, Cindy APPLICANT: Smith, Craig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Method of Tre
                                                                                                                       187 VVAI----PGNASMDAVCT 201
                                                                                                                                                        168 TFGLLLIQKGNATHDNVCS 186
                                                                                                                                                                                                                             114 EI-----EFCLKHRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCS 167
                                                                                                                                                                                            127 ALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICN
                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                               67 CTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTCRPGWYC 126
                                                                                                                                                                                                                                                                                                  54 CTVRRKTLCVPCPDHSYTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVCECEEGRYL 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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amino acid
                                Application US/08650000
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51 University Street
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Method of Treating
The Translation Using
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Tumor Necrosi
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NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:

ADDRESSEE:

Immunex Corporation

Street

COUNTRY:

51 University Seattle Washington

U.S.A.

CITLE OF INVENTION:

Tumor Necrosis Factor Receptors

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RESULT 9
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 405,370
FILING DATE: 11-SEP-989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 421,417
FILING DATE: 13-OCT-1989
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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NAME: Wight, Christopher L.
REGISTRATION UNMER: 31,680
REFERENCE/DOCKET NUMBER: 2501-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER:
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                                                                                   187 VVAI----PGNASMDAVCT
                                                                                                                         168 TFGLLLIQKGNATHDNVCS 186
                                                                                                                                                                                                            114 EI-----EFCLKHRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCS 167
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                                                                                                                                                                                                                                                                                              54 CTVRRKTLCVPCPDHSYTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVCECEEGRYL 113
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                                                                                                                                                                                                                                                                                                                                        9 ALAYGLEL - - WAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVF 66
                                                                                                                                                                                                                                                                                                                                                                                  8 ALLVLLDIIEWTTQETLPPK--YLHYDPETGH-------
                                                                                                                                                                   ALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICN 186
                                                                                                                                                                                                                                                      CTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTCRPGWYC 126
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; TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS FACTOR-a AND
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Best Local S
Matches 69
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07
FILING DATE: 10-MAY-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                     APPLICATION NUMBER: US
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
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                                                                                                                                                     COMPUTER: TEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Smith, Craig A.
APPLICANT: Goodwin, Raymond G.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Tumor Necrosis Factor Receptors
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CITY: Seattle
                                                                                                                                                                                                                                                                             STATE: Washington COUNTRY: U.S.A. ZIP: 98101
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FILING DATE:
APPLICATION NUMBER:
FILING DATE:
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                  us/08/038,765
                                                          US/08/468,453
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PRIOR APPLICATION DATA:

APPLICATION NUMBER:

APPLICATION NUMBER:

11-SEP-1989

US 405,370

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                                                                                  5395760-4
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                                                                                                                       SEQ ID
Query Match
Best Local Similarity
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Best Local
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APPLICANT: SMITH, CRAIG A., GOODWIN, RAYMOND G., BECKMANN
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 421,417
FILING DATE: 13-OCT-1989
                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 17
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
OF THE PRIOR APPLICATION NIMBER: US 421,417
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REFERENCE/DOCKET NUMBER: 250
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               163 HTNCSTFGLLLIQKGNATHDNVCS 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 GRYCALKTHSGSCROCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTFSDTTSSTDVCRP 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110 GRYLEIEF------CLKHRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIK 162
                                                                                                                                                               APPLICATION NUMBER: 405,370 FILING DATE: 11-SEP-1989 APPLICATION NUMBER: 403,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 Match 14.3%; Score 312; DB 2; Local Similarity 34.3%; Pred. No. 3.8e-21 nes 70; Conservative 22; Mismatches 8
                                                                                                   NO:4:
LENGTH: 474
                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/
FILING DATE: 10-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50 LKQHCTVRRKTLCVPCPDHSYTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVCECEE 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 VKHFCNKTSDTVCADCEASMYTQVWNQFRTCLSCSSSCTTDQVEIRACTKQQNRVCACEA 123
                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 LWVALVFELQL--WATGHTVPAQVVLTPYKPEPGYECQISQEYYDRKAQMCCAKCPPGQY 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     474 amino acids
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14.3%;
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Score 312; DB 5; Pred. No. 3.8e-21;
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                   Length 474;
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Local Similarity les 69; Conser

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                                                                                                      US-08-243-010-1
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                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/798,564
FILING DATE: 26-NOV-1991
APPLICATION NUMBER: DE P 40 37 837.3
FILING DATE: 28-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Elnaudi, Carol P.
REGISTRATION NUMBER: 32,220
REGERENCE/DOCKET NUMBER: 02481-1132-000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                         TELEFAX: 202-408-4400 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 13-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 GRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTFSDTTSSTDVCRP 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 HRICS----ILAIPGNASTDAVCA 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 GRYLEIEF-----CLKHRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163 HTNCSTFGLLLIQKGNATHDNVCS 186
                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Finnegan, Henderson, Farabow, Garrett ADDRESSEE: Dunner STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50 LKQHCTVRRKTLCVPCPDHSYTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVCECEE 109
                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 VKHFCNKTSDTVCADCEASMYTQVWNQFRTCLSCSSSCTTDQVEIRACTKQQNRVCACEA 123
                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 LCCALLVLLDIIEWTTQETLPPKYL--HYDPETGH------QLLCDKCAPGTY 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LWVALVFELQL--WATGHTVPAQVVLTPYKPEPGYECQISQEYYDRKAQMCCAKCPPGQY 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70;
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5639597
                                                                                                                                                                                     486 amino acids
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                                                                                                                       peptide
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Cell-free Receptor Binding Assays, The
Production and Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Release #1.0, Version #1.
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                                                                                                                                                                                                                                                                                                                  02481-1132-00000
Score 312; DB 1;
Pred. No. 3.9e-21;
9; Mismatches 85;
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                                      Length 486;
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                                                                                                                                        Query Match
Best Local Similarity
Matches 69; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Wight, Christopher L.
REGISTRATION UNBER: 31,680
                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Method of Treating TNF-Dependent
TITLE OF INVENTION: Inflammation Using Tumor Necrosis Factor Antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: __
STREET: __
Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 EI-----EFCLKHRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCS 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168 TFGLLLIQKGNATHDNVCS 186
 96
                                54 CTVRRKTLCVPCPDHSYTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVCECEEGRYL 113
                                                                     38
                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/07/946,236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67
                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                  LENGTH:
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CTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTCRPGWYC 155
                                                                                                    ALLVLLDIIEWTTQETLPPK--YLHYDPETGH------QLLCDKCAPGTYLKQH 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTCRPGWYC 126
                                                                     ALAVGLEL - - WAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVF 95
                                                                                                                                                                                                                                                                              amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 University Street
                                                                                                                                                                                                                                                                                                                                                       (206)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U.S.A.
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Smith, Craig A.
                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                     (206) 587-0430
206) 587-0606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunex Corporation
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                                                                                                                                                       14.38;
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                                                                                                                                       19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        2503
                                                                                                                                                       Score 312; DB 1;
Pred. No. 4.3e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Version #1.25
                                                                                                                                          85
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                                                                                                                                                                       Length 518;
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; MOLECULE TYPE:
US-08-959-382-2
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GENERAL INFORMATION:
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                                                                                                                                                                                                             Martches
                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 846169
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/04
FILING DATE: 02-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/959,382
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER & PRESTIA
STREET: P.O. BOX 980
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 610-407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Tumor Necrosis Related Receptor.
TITLE OF INVENTION: TR7
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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150 CPVGWGVRKKGTETEDVRCKQCARGTFSDVPSSVMKCKAYTDCLSQNLVVIKPGTKETDN 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                124 CPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNATHDN 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: P.U. --
                                                                                            64 PCPDHSYTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVCECEEGRYLEIEFCLKHRS 123
                                                                                                                                        30 LLLLGFLSTTTAQPEQKASNLIGTYRHVDRATGQVLTCDKCPAGTYVSEHCTNTSLRVCS 89
                                                                                                                                                                        10 LYLLDIIEWTTQE-----TLPPKYLHYDPETGHQLLCDKCAPGTYLKQHCTVRRKTLCV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 28-OC
                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 655 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
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                                                                   SCPVGTFTRHENGIEKCHDCSQPCPWPMIEKLPCAALTDRECTCPPGMFQSNATCAPHTV 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALSKQEGERLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICN
                                                                                                                                                                                                              91;
                                                                                                                                                                                                                             Similarity
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YOUNG, PETER
                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                 protein
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Pred. No. 5.7e-20;
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US-08-219-237B-5
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                                                                                                                                                                                                                                                                                         Query Match 13.6%; Score 297; DB 2; Length 163; Best Local Similarity 36.8%; Pred. No. 2.1e-20; Matches 60; Conservative 17; Mismatches 74; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/08219237B Patent No. 5874546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 1
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 163 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 28-MAR-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/872,129

FILING DATE: 22-APR-1992

CLASSIFICATION: 435

ATTORNEY/ACENT INFORMATION:
NAME: James W. Hellwege
REGISTRATION NUMBER: 28,808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: NAGATA, Shigekazu
APPLICANT: ITOH, Naoto
APPLICANT: YONEHARA, Shin
TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/219,237B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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125 PCAPGTFSNTTSSTDICRPHQICNVVAI----PGNASMDAVCT 163
                                    144 KCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNATHDNVCS 186
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STREET: P.O. Box 2266 Eads Station
CITY: Arlington
STATE: Virginia
COUNTRY: USA
                                                                                              65 DOVETOACTREONRICTCRPGWYCALSKOEGCRLCAPLRKCRPGFGVARPGTETSDVVCK 124
                                                                                                                                90 LQSVKQECNRTHNRVCECEEGRYLEI-----EFCLKHRSCPPGSGVVQAGTPERNTVCK 143
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Search completed: December 27, 2000, 10:53:53
Job time: 144 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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008727 rattus norv
0987144 mus musculu
095407 homo sapien
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062327 musi musculu
016042 homo sapien
088734 mus musculu
075509 homo sapien
08934 mus musculu
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057100 monkeypox v
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ALIGNMENTS

RP SEQUENCE FROM N.A. RP SEQUENCE FROM N.A. RC TISSUE-PLACENTA; RX MEDLINE; 98351569. RA Morinaga T., Nakagawa N., Yasuda H., Tsuda	Identity of steoclastogenesis osteoproteg.in (OPG): a mechani osteoclastogenesis in vitro. Endocrinology 139:1329-1337(1998	NCE FROM N.A. E-LUNG FIBROBLAST; NE; 98151033. A. H., Shima N., Nakagawa N. Goto M., Yamaguchi K., Y., Goto M., Yamaguchi K., F. Morinaga T. Higashi	RA Sugys 5., Boyle W.J.; RT Osteoprotegerin: a novel secreted protein RT of bone density."; RL Cell 89:309-319(1997). RN [2]	Luethy K., Mouyen H.O., Wooden S., Derose M., Elliott R., Colombero A., Davy E., Bucay N., Renshaw-Gegg L., Campbell P., Sander S., Van G., Tar	C. R.,	INFRSTILE OK OPG OK OCLE. Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;	01-JUL-1997 (TEMBLEE). 04, Creat 01-JUL-1997 (TEMBLEE). 04, Last 01-MAY-2000 (TEMBLEE). 13, Last 0STEOPROTEGERIN PRECURSOR (OSTEOO (OCIF) (TUMOR NECROSIS FACTOR REC	SULT 1
da E., Higashio K.;	inhibitory factor (OCIF) and inhibitory factor (OCIF) and sm by which OPG/OCIF inhibits	., Mochizuki SI., Yano K., Fujise N., Kuriyama M., Kanno T., Murakami A., K	in involved in the regulation	Bennett L., Boone T., Shinamoto G., , Tan HL., Trail G., Sullivan J., Hughes T.M., Hill D., Pattison W., pley J., Derby P., Lee R.,	Kelley M., Chang MS.,	Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.	Led) sequence update) annotation update) LASTOCENESIS INHIBITORY FACTOR) TEPTOR SUPERFAMILY MEMBER 11B).	AA.

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RESULT
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Best Local Similarity 99.4%;
Matches 173; Conservative
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Eur. J. Biochem. 254:685-691(1998).
-:- FUNCTION: MAY REGULATE BONE RESORPTION BY
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PROSITE; PS00652; TNFR_NGFR_1;
PROSITE; PS50050; TNFR_NGFR_2;
Glycoprotein; Repeat; Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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-!- SUBCELLULAR.

-!- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN LUNG, H
KIDNEY, PLACENTA, THYROID, SPINAL CORD AND LIVER. ALSO DET
A NUMBER OF OTHER HEMATOPOLETIC AND IMMURE ORGANS. NOT DET
THE PANCREAS OR PERIPHERAL BLOOD LYMPHOCYTES.
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REG
EMBL; AB00812; BAA32076.1; --
EMBL; AB00882; BAA32076.1; --
EMBL; BA00882; BAA32076.1; --
EMBL; BAO332; AAB53709.1; --
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SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY
                                                                                                                                                                                                                                    VCKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQK
                                                                                                                                                                                                                                                                                                                        KETFPPKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDEC
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  (TrEMBLrel. 13,
                                              PRELIMINARY;
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
                                                                                                                                                                                                                                                                                                                                                                                                            Score 1009; DB 4;
Pred. No. 6.6e-80;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).

Bukaryota; Metazoa; Chordata;

Eukaryota; Metazoa; Rodentia;
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Homo sapiens (Human).
Homo sapiens (Human).
horia; Metazoa; Chordata: (horia; Primates;
   gene
Gene
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Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S., Luethy R., Nguyen H.O., Wooden S., Bennett L., Boone T., Shimamoto Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R., Suggs S., Boyle W.J.;
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SEQUENCE
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Sheng Wu Hua Hsueh Yu Sheng
EMBL; AF134187; AAF20168.1;
INTERPRO; IPRO01368; -.
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"Structure of the mouse gene and its expression Gene 215:339-343(1998).
                                                                                          Mizuno A., M
Higashio K.;
                                                                                                                                                        STRAIN-129/OLA, A MEDLINE; 98382527
                                                                                                                                                                                                                                                                                "Osteoprotegerin: a novel secreted of bone density."; Cell 89:309-319(1997).
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PROSITE; PS00652; TNFR_NGFR_1;
PROSITE; PS50050; TNFR_NGFR_2;
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on of Osteoprotegerin
Sheng Wu Wu Li Hsueh
                                in embryogenesis.";
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                                                                                                                           Nakagawa
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4, Last sequence update)
3, Last annotation update)
(OSTEOCLASTOGENESIS INHIBITORY FACTOR)
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Pred. No. 7.4e-80;
0; Mismatches 0;
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Sciurognathi;
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thi; Muridae; Murinae; Mus
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31:680-684(1999).
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Best Local S
Matches 151
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MGD; MGI:109587; Opg.
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INTERPRO; IPR001388; -.
PFAM; PF00020; TNFR_C6; 3
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SIGNAL
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PROSITE; PS50017; DEATH_DOMAIN; 1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
Glycoprotein; Repeat; Cytokine; Signal.
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 18
                                21
                                                                 Local Similarity
nes 151; Conserv
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SUBUNIT: HOMODINER (MAJOR FORM) AND MONOMER (MINOR FORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BRAIN, HEART, KIDNEY, S
PLACENTA. NOT DETECTED
                                                                                                                                                                                                                                                                                                                                                                                                                                    AB013898; BAA28269.1;
AB0139903; BAA33388.1;
AB013899; BAA33388.1;
AB013900; BAA33388.1;
AB013901; BAA33388.1;
AB013902; BAA33388.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE
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                               DAY 7. AT DAY 11,
5 TO DAY 17.
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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RI Cell 89:309:319(1997).

RI Cell STEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY CONTINUES BY INTEROPTING CELL-TO-CELL SIGNALING BETWEEN CONTENCESIS BY INTEROPTING CONTENCESIS CONTENCESIS BY INTEROPTING CONTENCESIS CONTENCESI
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Luethy R., Nguyen H.O., Wooden S., Bennett L., Boone T
Derose M., Elliott R., Colombero A., Tan H.-L., Trail
Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill
Campbell P., Sander S., Van G., Tarpley J., Derby P.,
Siggs S., Bovle W T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus ()
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.I
TISSUE=INTESTINE;
MEDLINE; 97262071
                                                                                                                                                                                                                                                                                                                             PROSITE; PS00552; TNFR_NGFR_1; PROSITE; PS50050; TNFR_NGFR_2; Glycoprotein; Repeat; Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Suggs S., Boyle W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OSTEOPROTEGERIN
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0 (TrEMBLrel. 13,
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Da; Chordata;
La; Rodentia;
                 46192
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04, Last sequence update)
13, Last annotation.update)
DR (CSTEOCLASTOGENESIS INHIBITORY
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BY SIMILAR
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TNFR-CYS
TNFR-CYS
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FEC6A31F1D4E573A CRC64;
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Sciurognathi; Muridae;
                                                                                Y SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                               UNKNOWN_1.
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one T., Shimamoto (
rail G., Sullivan (
Hill D., Pattison V
P., Lee R.,
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; Murinae; Rat
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Best Local :
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SEQUENCE
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"Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a single chain antibody (scFV).";
Submitted (MAX-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF152372; AAD40243.1; ...
INTERPRO; IPR003006; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation updat
GAMMA1 HEAVY CHAIN OF MAB7 (FRACMENT).
Mus_musculus (Mouse).
                                       DCR3
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PROSITE; PS00290; IG_MHC; UNKNOWN_1
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Mammalia; Eutheria; Rodentia;
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                                  OR TR6.
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TNFR_NGFR_1; UNKNOWN_1.

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Matches 69
                                                                                                                                                                                                                                                                                                                                                                                                                   OSPUSO; PRELIMINARY;
OSPUSO;
01-MAY-2000 (TIEMBLIEL 1
01-MAY-2000 (TIEMBLIEL 1
01-JUN-2000 (TIEMBLIEL 1
                                                                                                                                                                                                                                                                               Salvelinus fontinalis (Brook trout).
Salvelinus fontinalis (Brook trout).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Actinopterygii; Neopterygii; Teleostei; Euteleostei
Prctacanthopterygii; Salmoniformes; Salmonidae; Sal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Receptor SEQUENCE
                                                                                                  Bobe J., Goetz F.W.;
"A tumor necrosis factor receptor he
trout (Salvelinus fontinalis) cvary
Biol. Reprod. 0:0-0(1999).
EMBL; AF156738; AAD56428.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yu K.Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon R. A newly identified member of tumor necrosis fact superfamily (TR6) suppresses Light-mediated apopt J. Biol. Chem. 274:13733-13736(1999).
EMBL: ABT104419; AADD20568.1; -...
EMBL: AF1044240, AADD29688.1; -...
EMBL: AF134240; AADD29688.1; -...
EMBL: AF134240; ADD29688.1; -...
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Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C., Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T., Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L., Goddard A.D., Botstein D., Ashkenazi A.; "Genomic amplification of a decoy receptor for Fas ligand in lung"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERPRO; IPR000561; -.
INTERPRO; IPR001368; -.
PFAM; PF00020; TNFR_C6; 4.
PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                              INTERPRO; IPR000561; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
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                           TNFR_c6; 4.
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Last sequence update)
Last annotation update)
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Pred. No. 5.4e-30;
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Best Local Similarity
Matches 64; Conserv
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Q62327;
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PROSITE; |
Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mamm. Genome 5:726-727(1994).
EMBL; X76401; CAA53981.1; -.
HSSP; P19438; INCF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAY-2000 (TrEMBLrel. 13, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR 2 MRNA (FRAGMENT).
                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERPRO; IPRO01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE;
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                    149
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                                                                                                                                                   31 YYDRKA--QMCCAKCPPGQYVKHFCNKTSDTVCADCEASMYTQVWNQFRTCLSCSSSCST 88
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mes 71; Conserv
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                                                                                                    LQYVKQECNRTHNRVCECKEGRYLEIEF------CLKHRSCPPGFGVVQAGTPERNTVC
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                    KACAPGTFSDTTSSTDVCRPHRICSILAI----PGNASTDAVCAPES
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                                                                                   DQVETRACTKQQNRVCACEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLC
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E: PS50050; TNFR_NGFR_2;
E: PS50050; TNFR_NGFR_2;
E: PS50050; TNFR_NGFR_2;
E: PS500652; TNFR_NGFR_1;
E: PS00652; TNFR_NGFR_2;
E: PS50050; TNFR_NGFR_1;
E: PS50050; TNFR_NGFR_2;
E: PS50050; TNFR_NGF
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PS50050; TNFR_NGFR_2; 1.
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38.3%;
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type 2 tumor
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                                                                                                                                                                                                                   Score 332.5; DB 11;
Pred. No. 4.9e-21;
0; Mismatches 70;
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necrosis factor receptor
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Best Local S
Matches 69
EMBL; Y14619; CAA74969.1; J
EMBL; Y14620; CAA74969.1; J
EMBL; Y14621; CAA74969.1; J
EMBL; Y14622; CAA74969.1; J
EMBL; Y14623; CAA74969.1; J
                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dembic Z., Loetscher H., (
Brockhaus M., Lesslauer W
                                                                                   Genomics 0:0-0(0)
                                                                                                  Characterization of the
                                                                                                                                     Hurle B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FRCM N.A. MEDLINE; 91570690.
                                                                                                                    The Mouse fumor
                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERPRO; IPR001368; -.
                                                                                                                                                                                                                                                                                                                                                                                                                           177
                                                                                                                                                                                                                                                                                                                                                                                                                                                          391
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                                                                                                                                   Segade F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        396
                                                                                                                                                                                                                                                                                                                                                                                                                         182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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088734
PKELLALL
088734;
088734;
088734;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TREMBLrel. 08, Last sequence update)
01-MAY-2000 (TREMBLrel. 13, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q16042 PRELIMINARY; PRT; 439 AA. 0.15042; O1-NOV-1996; (TIEMBLrel. 01, Created) O1-JAN-1999 (TIEMBLrel. 09, Last sequence update) O1-MAY-2000 (TIEMBLrel. 13, Last annotation update TUMOR NECROSIS FACTOR RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HORO sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM; PF00020; TNFR_C6; 4.
PF0051TE; PS00652; TNFR_NGFR_1;
PF0051TE; PS50050; TNFR_NGFR_2;
SEQUENCE 439 AA; 46090 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Two human TNF receptors have similar intracellular, domain sequences."; Cytokine 2:231-237(1990).
EMBL; S63368; AAB19824.1; -.
HSSP; P25942; ICDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               331 CPPGFGVVQAGTPERNTVCKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDN 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGKETFPP-----KYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAI----PGNASMDA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRK, 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YTDSWHTSDECLYCSPVCKELQYVKQECNRTHNRVCECKEGRYLEI-----EFCLKHRS 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAQVAFTPYAPEPGSTCRLREYYDQTA-QMCCSKCSPGQHAKVFCTKTSDTVCDSCEDST 60
                                                                                                                                  F., Rodriguez R., Ramos S.S., Lazo P.S.;
Necrosis Factor Receptor Gene:Genomic St
of the two Transcripts.";
                                                                                                                                                                                                                                                    Chordata;
Rodentia;
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JOINED.
JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 331; DB 4;
Pred. No. 6.3e-21;
8; Mismatches 79;
                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ωΝ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   extracellular, but distinct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Y.C., Lahm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             update)
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                                                                                                                                                              Structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
                                                                                                                                                                                                                                                      Mus
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075509
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Best Local S
Matches 75
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INTERPRO: IPROUZO: TNFR_c6; 4.
PFAM; PF00020; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 3.
PROUENCE 482 AA; 51106 MW; F
                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF068868; AAC34583.1; ...
INTERPRO; IPR000488; ...
INTERPRO; IPR001368; ...
PFAM; PF00020; TNFR_C6; 4.
PFAM; PF00531; death; 1.
PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50017; DEATH_DOMAIN; 1.
PROSITE; PS50050; TNFR_NGFR_2; 1.
SEQUENCE 655 AA; 71844 MW; 48939391C485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O75509 PRELIMINARY; PRT; 655 AA.
O75509;
O1-NOV-1998 (TrEMBLrel. 08, Created)
O1-NOV-1998 (TrEMBLrel. 08, Last sequence update)
O1-MAY-2000 (TrEMBLrel. 13, Last annotation update)
TNFR-RELATED DEATH RECEPTOR-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pan G., Bauer J.H., Haridas V., Wang S., Liu D., Ni J., Vincenz C., Aggarwal B.B., Dixit V.M.; "Identification and functional characterization of DR6, domain containing TNF receptor."; Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Y14679;
HSSP; P19438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
                                                         114
                                                                                                                                                                                                             235 YLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVC 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241
   355
                                                                                                                  295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187 LYSKLTYDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKETFPPKY-----LHYDE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108
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GFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNIC 392
                                                                                                            KELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRCPD 354
                                                   PWPMIEKLPCAALTDRECTCPPGMFQSNATCAPHTVCPVGWGVRKKGTETEDVRCKQCAR 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VLCKACAPGTFSDTTSSTDVCRPHRICSILAI - - - - PGNASTDAVCAPES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CKELQYVKOECNRTHNRVCECKEGRYLEIEF------CLKHRSCPPGFGVVQAGTPERN 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YRHVDRATGQVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTRHENGIEKCHDCSQPC 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CSTDQVETRACTKQQNRVCACEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ETSHQLLCDKCPPGTYLKQHCT-----AKWKTVCAPCPDHYYTDSWHTSDECLYCSPV 293
                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                   12.8%;
35.4%;
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                                                                                                                                                                                                                                                                                                                   Score 287; DB 4;
Pred. No. 6.8e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 327;
Pred. No. 1.
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; 3.
F6C15046B48FF83C (
                                                                                                                                                                                                                                                                                                                                                                                                                                            48939391C4852A33 CRC64;
                                                                                                                                                                                                                                                                                        Mismatches
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.6e-20;
                                                                                                                                                                                                                                                                                        81;
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                                                                                                                                                                                                                                                                                                                                           Length 655;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ni J., Yu G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                novel
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                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                  Gaps
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RESULT 13
Q90544
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Q9UP60
ID Q9U
AC Q9U
   RRRR RRC OCC OCT DT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        regulated in colorectal cancer."
Submitted (JUN-1998) to the EMBL,
EMBL; AR667420; AAC19365.1; -.
INTERPRO; IPRO00495; -.
INTERPRO; IPRO03006; -.
INTERPRO; IPRO03006; -.
PFAM; PF00047; 19; 3.
PFONSITE; PS00290; IG_MHC; UNKNOW;
PROSITE; PS00290; IG_MHC; UNKNOW;
SEQUENCE 384 AA; 40947 MW; B
TISSUE=SPLEEN;
MEDLINE; 95183140.
Greenberg A.S., Avi
Flajnik M.F.;
                                                                                                   NOVEL ANTIGEN RECEPTOR PRECUESOR.
Ginglymostoma cirratum (Nurse shark).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; C
Elasmobranchii; Neoselachii; Galeomorphii; Galeoidea;
                                                                                                                                                                                                       Q90544
Q90544;
                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

Zheng S., Cao J., Cao W., Cai X., Ger

Identification and characterization

"Identification for a characterization",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9UP60;
01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-JUN-2000 (TrEMBLrel.
                                                         SEQUENCE FROM N.A.
                                                                                    Orectolobiformes; Ginglymostomatidae; Ginglymostoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9UP60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174
                                                                                                                                                                                                                                                                                              354 AFTQKTIDRLAGKPT
                                                                                                                                                                                                                                                                                                                                                                                161 EWESNGQ--PENNYKTTPPVLD-SDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN
                                                                                                                                                                                                                                                                                                                                                                                                                                          102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178
                                                                                                                                                                                                                                                                                                                         216 HYTQKSLSLSPGKET 230
                                                                                                                                                                                                                                                                                                                                                    294 RWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPL
                                                                                                                                                                                                                                                                                                                                                                                                              235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KHYTNPSQDVTVPCPVPSTPPTPSPST-PPTPSPSCCHPRLSLHRPALEDLLLGSEANLT
                                                                                                                                                                                                                                                                                                                                                                                                              CTAAYPESKTPLTATLSKS-GNTFRPEVHLLPPPSEELALNELVTLTCLARGFSPKDVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KTHTCP-----PCPAPELLGGPSVFLFPPKPK-------DTLMISRTPEVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80; Conservative
                                                                                                                                                                                                                       PRELIMINARY;
                Avila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.3%;
                                                                                                                                                                                                                                                                                              368
                D.,
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MW; BA7ADC3CA5A9DD48
               Hughes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 276; DB 4; I
; Pred. No. 3.2e-16;
33; Mismatches 110;
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Last sequence update)
Last annotation updat
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X
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ion of SNC73,
               Hughes
                                                                                                                                                                                                                         684
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                                                                                                                                                            update)
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                McKinney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRC64
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                                                                                                                    Chondrichthyes;
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RT RT RT DR DR DR DR DR DR FT FT SQ

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RESULT
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AC QO
DT QO
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Best Local S
Matches 71
  PFAM; PF00020; TNFR_C6; 4.

PROSITE; PS00052; TNFR_NGFR_2; 1

PROSITE; PS50050; TNFR_NGFR_2; 1

Receptor; Glycoprotein; Transmem 1 2 POT 2 POT 2 REC CHAIN 23 616 REC DOMAIN 24 212 EXT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNERSFILA OR KALL...
Homo saplens (Human).
Homo saplens (Human).
Thereof the control of the cont
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Signal
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 98032977.
Anderson D.M., Maraskovsky
Tometsko M.E., Roux E.R., T
Galibert L.;
"A homologue of the TNF rec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 13, Last annotation update)
RECEPTOR ACTIVATOR OF NF-KAPPA-B PRECURSOR (TNF-RELATED INDUCED CYTOKINE RECEPTOR) (RANK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A new antigen receptor gene family that undergoes rearrangement and extensive somatic diversification in sharks.";
Nature 374:168-173(1995).
REMBL; U18701; AAA8195.1; -.
INTERPRO; IPRO00455; -.
INTERPRO; IPRO03006; -.
PERAM; PF00047; 19; 6 USC. INVENEE Concepts.
                                                                                                                                                                                                                                                                                          and dendritic-cell function.";

Nature 390:175-179(1997).

-I- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS RANKL.

-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).

-I- TISSUE SPECIFICITY: UBIQUITOUS EXPRESSION WITH HIGH LEVELS SKELETAL MUSCLE, THYMUS, LIVER, COLON, SMALL INTESTINE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9Y6Q6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE; 98032977.
                                                                                                                                                                                                     EMBL; AF018253; MIM; 603499; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00290;
                                                                                                                                                                              INTERPRO; IPR001368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   196
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                                                                                                                                                                                                                                                                                                                                                                                                                      homologue of the TNF receptor dendritic-cell function.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14
                                                                                                                                                                                                                                                SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EL-TKNQVSLTCLVKGFYPSDIAVEWESNGQ-PENNYKTTPPVLDSDGSFFLYSKLTVDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE-VKFNWYVDGVEVHNAKTKPREEQYN 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEWNSDTTYSCLVGHPSL-NRDLIRSTNKSNGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK-GQPREPQVYTLPPSRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYSTLKP-PFEEIWTQQTATIYCEIY---YSDLENIKYFWQVNGVERKKGVETQNPEWSG
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684
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AAB86809.
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IG_MHC;
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684
75224
                                                                         Transmembrane; Signal;
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                                                                                                                                                                                                                         LA-NGFR/TNFR-TYPE CYSTEINE-RICH; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35;
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Pred. No. 1.3e-15;
5; Mismatches 98;
POTENTIAL.

RECEPTOR ACTIVATOR OF NF-KAPPA-B
EXTRACELLULAR (POTENTIAL).
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2FF9D2071CDA6DFD CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; F
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Billingsley W.L., D
e M.C., DuBose R.F.,
                                                                                                                         UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             and
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                                                                                                                                                                                                                                                                                                                                                                                                                                             enhance
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo
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                                                                                                                                                                                                                                             REGION.
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ADRENAL
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RESULT
035305
TD 035305
035305;
11.JAN
 Query Match
Best Local S
Matches 56
                                                                                                                                                                                                                                                 TISSUE-LIVER EPITHELIUM;
MEDLINE; 98032977.
Anderson D.P., Maraskovsk.
Tometsko M.E., Roux E.R.,
Galibert L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
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DOMAIN
DOMAIN
                                   INTERPRO;
INTERPRO;
PFAM; PFOC
                                              and dendritic-cell function.";

Nature 390:175-179(1997).

-:- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS RANKL.
-:- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL)
-:- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REBENGL; AF019046; AAB86810.1; -.
HSSP; P25942; 1CDF.
HSSP; P25942; 1CDF.
MGD; MGI:3314891; Tnfrsfila.
INTERPRO; IPR000561; -.
INTERPRO; IPR001368; -.
                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1998 (TIEMBLIEL. 05, Created)
01-JAN-1998 (TIEMBLIEL. 05, Last sequence up
01-MAY-2000 (TIEMBLIEL. 13, Last annotation
RECEPTOR ACTIVATOR OF NF-KAPPA-B PRECURSOR (
INDUCED CYTOKINE RECEPTOR) (RANK).
TINFRSF11A OR RANK.
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CARBOHYD
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REPEAT
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                                                                                                                                                                                                                                  homologue of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVC---KELQYVKQEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STDKCRPWINCIFLGKRVEHHGIEKSDAVCSSS
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 PS00652;
PS01186;
                                                                                                                                                                                                                                                                                                                                                          Metazoa; Chordata; C
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Roux E.R., 1
TNFR_NGFR_1; UNK
EGF_2; UNKNOWN_1
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36.6%;
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BY SIMILARITY.

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Pred. No. 6.3e-14;
7; Mismatches 73
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Sciurognathi; Muridae;
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Search completed: December 27, 2000, 10:52:42

Job time: 73 sec .
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                                                                                                                                                                                                                                                                                                                            106 NHTAPRRCACTAGYHWNSDCECCRRNTECAPGFGAQHPLQLNKDTVCTPCLLGFFSDVFS 165
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Gapop 10.0 , Gapext 0.5
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ALIGNMENTS

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	•	SEQUENCE (MYELOMA PROTEIN NIE). MEDLINE; 77070269. MEDLINE; 77070269. PONSTLING! H., Hilschmann N.; "The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure."; Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).		SEQUENCE OF 1-135 (MYELOMA PROTEIN EU). MEDLINE; 71064024. Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D., Waxdal M.J., Edelman G.M.; "The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4."; Biochemistry 9:3161-3170(1970).	[1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE; 82274238. Ellison J.W., Berson B.J., Hoc Ellison J.W., Berson B.J., Hoc Pitter and Sequence of a Nucleic Acids Res. 10:4071-407	1_HUMAN GC1_ PO18 21-J 21-J 15-J IG G IGHG HOMO Euka	RESULT 1

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"Rule of antibody structure. The primary structure of a monoclonal 1961 immunoglobulin (myeloma protein Nie), I: Purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";
Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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INTERPRO; IPR003006; -.
PFAM; PF00047; ig; 3.
PROSITE; PS00290; IG_MHC;
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Biochemistry 20:2361-2370(1981).
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; 1FC1; 15-JUL-92.
; 1FC2; 15-JUL-92.
; 147100; -
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35,116,198,269 EV ALSO DIFFERS I 155, 166, 177, 195, 198, 269, AN
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K -> R (IN G1M(3) MARKER).

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D -> E (IN G1M(NON-1) MARKER)
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L -> M (IN G1M(NON-1) MARKER).
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Best Local Similarity
Matches 227; Conserv
SEQUENCE OF 1-325 (
MEDLINE; 81007873.
Wang A.-C., Tung E.
"The primary struct
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Homo sapiens (Human).
Homo sapiens (Human).
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'--rvota; Primates;
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"Linkage and sequence homology of two human immu heavy chain constant region genes.";
proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982)
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evolutionary, and functional implications."; J. Immunol. 125:1048-1054(1980).

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132-325 (MYELOMA PROTEIN ZIE).

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EMBL; V00554; CAA23816.1; -.
EMBL; V00554; CAA23817.1; -.
PIR; A02148; G2HU.
MIM; 147110; -.
INTERPRO; IPR000495; -.
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PFAM; PF00047; 1g; 3.
PROSITE; PS00290; IG_MHC; 2.
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MEDLINE; 95255298.
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can. J. Blochem. 57:758-767(1979).
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MEDLINE; 83157104.
Ellison J.W., Buxbaum J
"Nucleotide sequence of
DNA 1:11-18(1981).
Immunoglobulin on NON_TER 1 DOMAIN 1 DOMAIN 99 DOMAIN 111
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P01861;
21-JUL-1986 (Rel. 01, Created)
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15-JUL-1999 (Rel. 38, Last annotation
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SEQUENCE (BIO21548.

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Michaelsen T.E., Frangione B.,
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21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
IG GAMMA-3 CHAIN C REGION (HEAVY CHAIN DISEASE PROTEIN) (HDC).
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ryota; Metazoa; Chordata;
alia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                               TO 59-289 OF PROTEIN WIS
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                                                                                                    Buxbaum J.N.;
                                                                                                                     Barritault D.,
                                                                                                                                                                  PROTEIN OMM).
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Pred. No. 5.4e
8; Mismatches
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                                                                             man:
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                                                                        cDNA sequence supports
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PFAM; PF00047; ig; 2
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MIM; 147120;
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MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL OF THE CHI REGION, AND PART OF THE HINGE COMPARED WITH NORMAL GAMMA-3 HEAVY CHAINS.

MISCELLANEOUS: DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM MISCELLANEOUS: DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM OR ANOTHER GAMMA CHAINS UBCLASS.

MISCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE TOENTICAL 15 RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11 NORMALLY PRESENT IN THE HINGE REGION.
MISCELLANDOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN.
MISCELLANDOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEGMENT (12-28).
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                                    MISSING (IN ZUC).
/FTId-VAR_003895.
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CH2.
CH3.
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F -> Y (IN OMM).
/FTId=VAR_003896.
E69CBC95705B2F46
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/FTId=VAR_003890.
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                                                                       /FTId=VAR_003893.
S -> N (IN OMM).
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Match
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SEQUENCE OF 132-161.
SEQUENCE OF 132-161.
MEDLINE; 70110015.
Fruchter R.G., Jackson S.A., Mole Fruchter R.G., Jackson S.A., Mole "Sequence studies of the Fd secti immunoglobulin G.";
niochem. J. 116:249-259(1970).
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MEDLINE; 84030930.
Bernstein K.E., Alexander
"Nucleotide sequence of a
F-I haplotype.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
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21-JUL-1986 (Rel. 01, Last seq
15-JUL-1999 (Rel. 38, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *Martens C.L., Moore K.W., Steinmetz M., Hood L., "Heavy chain genes of rabbit Ig0: isolation of a heavy chain and identification of two genomic C g proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 88-266 FROM MEDLINE; 83299917.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Sequence studies on the constant region immunoglobulin G of different allotype."; siochem. J. 151:337-349(1975).
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MEDLINE; 76135469.
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13; Mismatches
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    RESULT 6
GC2_CAVPO
ID GC2_C
AC P0186
AC P0186
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Best Local Sir
Matches 167;
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P01862;
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CON
SEQUENCE OF 4-68.

MEDLINE; 71058471.

Birshtein B.K., Hussain Q.Z., C
"Structure of heavy chain from immunoglobulin-G(2). 3. Amino a
                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
IG GAMMA-2 CHAIN C REGION.
Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
                                                                                                                                            Submitted
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                                                                                                                                                                                                                                    Mammalia;
                                                                                                                                                                  EQUENCE OF 1-3.
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A02161; GHRB.
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Similarity 71.7%;
57; Conservative 2
                                                                                                                                                                                                                                  ; Metazoa;
Eutheria;
                                                                                                                                          1 T.M.;
(APR-1975)
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Chordata;
Rodentia;
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    , Cebra J.J.;
om strain 13 gui;
o acid sequence ;
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modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                             PAVLDSDGSYFLYNKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 918.5; DB 1;
Pred. No. 5.4e-57;
9; Mismatches 32;
                                                                                                            Craniata; Vertebrata; Eut
Hystricognathi; Caviidae;
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3 AND 4).
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region
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Best Local
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                                                                                                                                                                                                                                      DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                         Oliveira B., Lamm M.E.;
"Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
Biochemistry 10:26-31(1971).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     half-cystine
Biochemistry
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                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                        PIR; A02151; G2GP.
INTERPRO; IPR000495; -.
INTERPRO; IPR003006; -.
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                                                                                                                                                                                                                                                                                                                                                                                                            DISULFIDE BONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                      Trischmann T.M., Cebra J.J.; ^{\prime\prime} Primary structure of the CH3 homology region from guinea pig IgG2 antibodies.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 227-311. MEDLINE; 75036073.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochemistry 13:4796-4803(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 7503
Tracey D.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 134-226.
MEDLINE; 75036072.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Structure of heavy chain from strain 13 guinea immunoglobulin-G(2). II. Amino acid sequence of and hinge region cyanogen bromide fragments."; Biochemistry 10:9-17(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Turner K.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 69-133 AND 312-329.
MEDLINE; 71058486.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Biochemistry
                                                                                                                                                                                                                                                                                               Immunoglobulin
                                                         126
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 286
                                      226
                   184
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                                    TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 65
SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                               TCPKCPPPENLGGPSVFIFPPKPKDTLMISLTPRVTCVVVDVSQDEPEVQFTWFVDNKPV 165
                                                                                                                                                     162;
                                                                                                                                                                                                                                                                                                                                                   INBRED GUINEA PIGS.
                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                       PS00290; IG_MHC; 1.
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                                                                                                                                                    Conservative
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72.3%;
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                                                                                                                                                   ; Score 889; DB 1;
; Pred. No. 6.1e-55;
24; Mismatches 36
                                                                                                                                                                                                                                      INTERCHAIN
INTERCHAIN
INTERCHAIN
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HEAVY
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RESULT 7

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Best Local
                                                                             GCB_RAT
P20761;
01-FEB-1991
01-FEB-1991
15-JUL-1999
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P22436;
01-AUG-1991 (Rel. 19
01-AUG-1991 (Rel. 19
15-JUL-1999 (Rel. 38
IG GAMMA-3 CHAIN C I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                   01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
IG GAMMA-2B CHAIN C REGION.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE; 85027161.

Wels J.A., Word C.J., Rimm D., Der-Balar

Tucker P.W., Blattner F.R.;

"Structural analysis of the murine IgG3

EMBO J. 3:2041-2046(1984).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; J00451; -; NOT_AN
PIR; B02156; G3MSC.
INTERPRO; IPR000495; -.
INTERPRO; IPR003006; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
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Immunoglobulin C region; Glycoprotein;
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38, Last annotation update)
REGION, SECRETED FORM.
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Rodentia;
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Pred. No. 6.3e-52;
4; Mismatches 37;
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HINGE.
CH2.
CH3.
  Craniata; Vertebrata; Sciurognathi; Muridae;
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Best Local Similarity 66.4
Matches 148; Conservative
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"Evolution of the rat imm
Gene 74:473-482(1988).

PIR; PS0018; PS0018.

INTERPRO; IPR000495; -.

INTERPRO; IPR003006; -.
                                                                         SEQUENCE FROM N.A.

MEDLINE; 85027161.

Wels J.A., Word C.J., Rimm D., Der-
Tucker P.W., Blattner F.R.;

"Structural analysis of the murine
EMBO J. 3:2041-2046(1984).
                                                                                                                                                     P03987;
23:OCT-1986 (Rel. 02, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG GAMMA-3 CHAIN C REGION, MEMBRANE-BOUND FORM.
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DISULFID
                                                     SEQUENCE |
                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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SEQUENCE FROM N.A.
MEDLINE; 89232738.
               Nucleic Acids
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PROSITE; PS00290; IG_MHC; 1.
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                             immunoglobulin
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Pred. No. 2.1e-51;
3; Mismatches 42
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Sciurognathi; Muridae;
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Matches 149
*Erueggemann M.;
*Evolution of the rat immur
Gene 74:473-482(1988).
PIR; PS0017; PS0017.
INTERPRO; IPR000495; -.
INTERPRO; IPR003006; -.
INTERPRO; IPR003006; -.
PFAM; PF00047; 19; 3
PROSITE; PS00290; IG_MHC; 1
Immunoglobulin domain; Immu
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EMBL; V01526; CAA24767.1; A
PIR; A02155; G3MSM.
INTERPRO; IPR000495; -
INTERPRO; IPR003006; -
PFAM; PF0047; 19; 3
PROSITE; PS00290; IG_MHC; 1
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P20759;
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SEQUENCE
                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
Mammalia; Eutheria; Rode
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15-JUL-1999 (Rel. 38, Last
IG GAMMA-1 CHAIN C REGION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane;
                                                                                                                          SEQUENCE FROM N.A. MEDLINE; 89232738.
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Transmembrane; Alternative
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Local Similarity 66.2%;
nes 149; Conservative 3
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QTPQYYTIPPPREQMSKKKVSLTCLVINFFSEAISVEWERNGELEQDYKNTPPILDSDGT 285
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Rodentia;
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E -> Q (IN REF. 2).
P -> F (IN REF. 2).
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Pred. No. 3.9e-51;
4; Mismatches 39;
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Sciurognathi; Muridae;
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Best Local Similarity
                                                                                                                                                          Honjo T., Obata M., Yamawaki-Katao Takahashi N., Mano Y.;
"Cloning and complete nucleotide st gamma 1 chain gene.";
Cell 18:559-568(1979).
[2]
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SEQUENCE FROM N.A.
MEDLINE; 80045036.
Honjo T., Obata M.,
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                                                                                      Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A. Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.; "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences cloned in a bacterial plasmid."; Gene 9:87-97(1980).
                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                           Rogers J., Clarke Sequence analysis heavy chain.";
                                    SEQUENCE OF 70-322 FROM N.A. MEDLINE; 80012837.
Rogers J., Clarke P., Salser Rogence analysis of cloned
                                                                                                                                        SEQUENCE OF 76-324 FROM N.A. MEDLINE; 80202559.
 SEQUENCE
                    Nucleic
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63.1%;
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Pred. No. 4.7e-50;
1; Mismatches 35
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Best Local Similarity
Matches 140; Conser
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MGD; MGI:96446; IGH-4.
INTERPRO; IPR000495; -
INTERPRO; IPR003006; -.
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           FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS
                                                                                      VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 124
                                                                                                                   YFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK
                                                                             VHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRP
                                      KAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMNTNGS
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Pred. No. 5.4e-50;
4; Mismatches 35
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domain.";
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Eukheria; Rodentia;
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Takahashi N., Mano Y.;
"Cloning and complete nucleotide sequence of
gamma 1 chain gene.";
Cell 18:559-568(1979).
                                           NON_TER
                                                                                                                                                                                           EMBL; V00793; CAA24172.1;
EMBL; V00793; CAA24173.1;
EMBL; V00793; CAA24174.1;
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"Nucleotide seguences of gene segments encoding membrane domains of immunoglobulin gamma chains.";
Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).

-i- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED GAMMA CHAINS. THE MAJOR SPECIES TO ENCODE MEMBRANE-BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Gene segments encoding transmembrane carboxyl termini of immunoglobulin gamma chains."; cell 26:19-27(1981).
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                                                                       Immunoglobulin domain; Immunoglobulin Alternative splicing; Transmembrane.
                                                                                                                                INTERPRO; IPR000495; -.
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Eisenberg D., Wall R
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[3]
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                                                                                                                                                                                                                                                                                                  Ol-FEB-1991 (Rel. 17, Created)
Ol-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG GAMMA-2C CHAIN C REGION.
                             NON_TER
                                                                                   EMBL; X07189; CAA30169.1;
PIR; S00847; S00847.
INTERPRO; IPRO00495; -.
                                                                                                                                                                                                  Brueggemann M., Delmastro-Galfre P., Waldmann H., Calak "Sequence of a rat immunoglobulin gamma 2c heavy chain region cDNA: extensive homology to mouse gamma 3."; Eur. J. Immunol. 18:317-319(1988).
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Eutheria; Rodentia;
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MOUSE
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for
Eur.
                                                                                                                                                                                                                                                                                                                                            "The complete nucleotide sequence of mouse and evolution of heavy chain genes: further sequence mediated domain transfer.";
            Bourgois A., Fougereau M., Rocca-Serra J.;
"Determination of the primary structure of a mouse IgG2a immunoglobulin:amino-acid sequence of the Fc fragment. Implic for the evolution of immunoglobulin structure and function.";
Eur. J. Biochem. 43:423-435(1974).
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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21-JUL-1986 (Rel. 01, Last seq
30-MAY-2000 (Rel. 39, Last ann
IG GAMMA-2A CHAIN C REGION, A
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Pred. No. 2e-49;
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Sciurognathi; Muridae;
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MOD_RES
SEQUENCE
                                                                                                                                                                          Mus musculus (Mouse).

Mus musculus (Mouse).
                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG GAMMA-2A CHAIN C REGION, MEMBRANE-BOUND FORM.
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de Preval C., Fougereau M.;

de Preval C., Fougereau M.;

"Determination of the primary structure of a mouse gamma G2a immunoglobulin. Identification of the disulfide bridges.";

Eur. J. Biochem. 30:452-462(1972).
          SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

WARDLINE; 82222190.

WARDAWAKI-KATAOKA Y., Nakai S., Miyata T., Honjo Yamawaki-Kataoka Y., Nakai S., Miyata Y., Miyata Y., Nakai S., Miyata Y., Nakai
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No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; J00471; AAB59661.1;
PIR; A02154; G2MSAM.
MGD; MGI:96443; IGH-1.
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INTERPRO; IPR003006; -.
PFAM; PF00047; 1g; 3.
PROSITE; PS00290; IG_MHC; 1.
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                                                                                                                                                                           Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
                                                       185 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 227
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MISCELLANEOUS: THE SEQUENCE OF RESIDUES 1-329 IS ASSUMED TO BE IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM OF
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RyFilpula, D.

RyFilpula, D.

Submitted to the EMBL Data Library, February 1993

A,Description: Screeing method for protein-protein

A:Reference number: S31866
                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig gamma-1 chain C region - synthetic
C;Species: synthetic
A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia col
C;Date: 06-dan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C;Accession: S31866
                                                                                                                                                                                 A;Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
C;Reywords: immunoglobulin
F;1-22/Region: Escherichia coli outer membrane protein A precursor
F;23-255/Region: human Ig gamma-1 chain C region
                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-255 <FIL>
                                                                                                                                                                                                                                                                                                                              A; Accession: S31866
                                                                                                                  Query Match
                                                                      Matches
                                                               Match 54.9%; So Local Similarity 100.0%; F
2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKENWYVD
                                                                 Score 1233; DB 4;
; Pred. No. 9.6e-72;
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                                                                                                                  Length 255;
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                                                                                                                                                                                                                                                                                                                                                                          of cloned gene produc
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                        61
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coli

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Ig gamma-1 chain C region - human (Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999 C; Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146 R; Ellison, J.W.; Berson, B.J.; Hood, L.E. Nucleic Acids Res. 10, 4071-4079, 1982 Nucleic Acids Res. 10, 4071-4079, 1982 A; Title: The nucleotide sequence of a human immunoglobulin C-gammal gene. A; Reference number: A93433; MUID:82274238 A; Accession: A93433
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A; Molecule type: protein
A; Molecule type: protein
A; Molecule: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330
A; Note: this sequence has the Glm(3) and Glm(non-1) markers
R; Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A; Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disu
A; Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disu
A; Contents: annotation; disulfide bonds
R; Contents: annotation; disulfide bonds
R; Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A; Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immuno enbromide cleavage products, and the disulfide bridges.
A; Reference number: A91667; MUID:77070267
A; Reichel, W. Hilschmann, N. Reference number: A91667; MUID:77070267
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A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E'
A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E'
A;Note: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met
R;Ponsting1, H; Hilschmann, N.
R;Ponsting1, H; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A;Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein
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A;Cross-references: GDB:120085;
A;Map position: 14q32.33-14q32.3
A;Introns: 99/1; 114/1; 224/1
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A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid A;Reference number: A90564; MUID:71064025
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A; Residues: 2-330 <HAR>
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Krounningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, Biochemistry 9, 3161-3170, 1970

A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequents;Reference number: A90563; MUID:71064024
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C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C:Superfamily: immunoglobulin C region; immunoglobulin homology C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F:20-85/Domain: immunoglobulin homology <IML>
F:317-206/Domain: immunoglobulin homology <IMS>
F:317-206/Domain: immunoglobulin homology <IMS>
F:317-83.144-204.250-308/Disulfide bonds: #status experimental F:103/Disulfide bonds: interchain (to light chain) #status experimental F:103/Disulfide bonds: interchain (to light chain) #status experimental
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Eur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human he
A;Reference number: S69339; MUID:95262687
A;Accession: S69339
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig heavy chain V region precursor - hum C:Species: Homo sapiens (man) C:Date: 19-Mar-1997 #sequence_revision C:Accession: S69339
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A;Residues: 1-374 <KHAD
A;Cross-references: EMBL:X81695
C;Superfamily: immunoglobulin C
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Matches 225; Conserv
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                                                                        268
                                                                                                                                               208 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
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les 227; Conservative
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                                                                                                                                                                  GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
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                      DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                         DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
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Pred. No. 3.
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submitted to the EMBL Data Library, September 1994
A; Reference number: S72664
A; Accession: S72664
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-374 < KNA>
A; Cross-references: EMBL:X81695
C; Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                               R; Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L. Mol. Immunol. 28, 319-322, 1991
A; Title: Nucleotide sequence of chimpanzee Fc A; Reference number: PT0207; MUID:91287716
Ccession: PT0207
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c;Species: Homo sapiens (man)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-2000
C;Accession: S72664
R;Khamlichi, A.A.
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Best Local (
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Mesidues: 1-234 <EHR>
Superfamily: immunoglobulin C
Keywords: immunoglobulin
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Best Local Similarity
Matches 225; Conserv
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 182
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                                                                                                                                                                          Local Similarity 98.0 ses 217; Conservative
                                                                                                                                         62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
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                                                                                                  DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSFGK 228
                                   GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYKTTPPVLDS
                                                         GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
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DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
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                                                                                                                                                                                                                                                   Score 1180; DB 2;
Pred. No. 2.1e-68;
1; Mismatches 2;
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Pred. No. 3.5e-71;
2; Mismatches 0;
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C; Supertamity: in C; Keywords: immur F; 20-85/Domain:
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A;Cross: references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: inmunoglobulin C region; immunoglobulin C;Keywords: inmunoglobulin C;Keywords: immunoglobulin homology <IMM>
                                                                                                                                                                                                        A;Title: A human immunoglobulin IGHG3 allele A;Reference number: A60764; MUID:90007613 A;Accession: A60764
                                                                                                                                                                                                                                                                                                                                                                                RESULT
A60764
                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
                                                                                                                                                                                                                                                                R; Huck, S.; Lefranc, G.; Lefranc, M.P. Immunogenetics 30, 250-257, 1989
                                                                                                                                                                                                                                                                                                   C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999 C;Accession: A60764
                                                                                                                                                                                                                                                                                                                                          Ig gamma-3 Chain C region, form LAT -
C; Species: Homo sapiens (man)
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A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain A;Reference number: A23511; MUID:86148507
A;Accession: A23511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig gamma-3 chain C region (allotype G3m(b)) - human
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
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A; Residues: 1-377 <HUC>
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Best Local Similarity 92.5
Matches 210; Conservative
                                                                                                              Superfamily: immunoglobulin C region; Keywords: immunoglobulin
   Matches
                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 DTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVD 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        271 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPPMLDS 330
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 210;
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                                                                                          immunoglobulin homology <IMM>
 Conservative
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92.5%;
                 50.9%;
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œ
Score 1144; DB 2;
Pred. No. 6.7e-66;
8; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                human
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                                   Length
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2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD

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A; Molecule type: protein
A; Residues: 1-19, (0',21-57,'z',59,'A',61-193,'D',195-325 <WAN>
A; Residues: 1-19, To near the complement-binding site
A; Note: Trp-156 is at or near the complement-binding site
R; Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
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A;Title: Structural studies of immunoglobulin G
A;Reference number: A93157; MUID:69064124
A;Contents: annotation; Sa, disulfide bonds
                                                       A; Contents: annotation; myeloma protein Sa, R; Frangione, B.; Milstein, C.; Pink, J.R.L. nature 221, 145-148, 1969
                                                                                                              R;Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain
A;Reference number: A90253; MUID:72033500
                                                                                                                                                                                                                                                           R; Hofmann, T.; Parr, D.M.
submitted to the Atlas, March
A; Reference number: A94591
                                                                                                                                                                                                                                                                                                                                                                                                  te: this sequence has since been revise revisement, T.; Parr, D.M.

Mol. Immunol. 16, 923-925, 1979

A;Title: A note on the amino acid sequence A;Reference number: A93132; MUID:80114419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: The amino acid sequences of the three A;Reference number: A90752; MUID:80001357 A;Contents: myeloma protein Zie A;Accession: A90752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Note: Lys-326 is probably removed posttranslationally R;Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A;Title: The primary structure of a human IgG2 heavy character number: Ay2809; MUID:81007873
A;Contents: myeloma protein Til
A;Accession: A92809
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                                                                                                                                                                                                                                               A; Contents:
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                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein
A; Residues: 238-275 < HOF>
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A; Residues: 1-326 <ELL>
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                                                                                                                                                                                                                                                                                                                                                                                 A;Contents: Zie
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esidues: 1-24,'E',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q'
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60-Ala
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A; MOLECULE 1-327 <ELLS
A; Residues: 1-327 <ELLS
A; Note: the sequence was determined from
R; Pink, J.R.L.; Buttery, S.H.; De Vries,
Riochem. J. 117, 33-47, 1970 anhiclasses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig gamma-4 chain C region - human C:Species: Homo sapiens (man) C:Date: 02-Apr-1982 #sequence_revision C:Accession: A9033; A90249; A02150 R;Ellison, J.; Buxbaum, J.; Hood, L. DNA 1, 11-18, 1981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: GDB:IGHG2
A;Cross-references: GDB:119338; OMIM:147110
A;Map position: 14932.33-14032.33
C;Complex: An immunoglobulin heterotetramer subunit consists of two hain disulfide bonds. In some cases, such as IgA and IgM, the subunit C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin C;Superfamily: immunoglobulin bomology C;Keywords: duplication; dlycoprotein; heterotetramer; immunoglobulin bomology C;Mayords: immunoglobulin c;D; immunoglobulin bomology C;Mayords: immunoglobulin c;D; immunoglo
                                                                                                                                                                                                               C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light hain disulfide bonds. In some cases, such as 1gA and 1gM, the subunits associate int C;Superfamily: immunoglobulin C region; immunoglobulin homology c;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                      A;Gene: GDB:IGHG4
A;Cross-references: GDB:119340; OI
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 111/1; 221/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochem. J. 117, 33-47, 1970
A;Title: Human immunoglobulin subiclasses.
A;Reference number: A90249; MUID:70207560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Nucleotide sequence
A;Reference number: A90933; M
A;Accession: A90933
A;Molecule type: DNA
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F;239-306/Domain: immunoglobulin homology <IM3>
F;239-306/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) *status experimental
F;27-83,140-200,246-304/Disulfide bonds: *status experimental
F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) *status
F;176/Binding site: carbohydrate (Asn) (covalent) *status predicted
                              F;134-203/Domain: immunoglobulin homology <IM2>F;240-307/Domain: immunoglobulin homology <IM3>F;14/Disulfide bonds: interchain (to light chair
                                                                                                                                          F:20-85/Domain: immunoglobulin homology <IM1>F:99-110/Region: hinge
   F;14/Disulfide bonds: interchain F;27-83,141-201,247-305/Disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein
A; Residues: 1-30;81-326 <PIN>
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MUID:83157104
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(to light chain) bonds: #status
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G.M.; Milstein,
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C;Species: Homo sapiens (man)
C;Date: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change
C;Accession: A90442; A92219; A90198; A93915; A02149
R;Frangione, B; Rosenwasser, E; Prelli, F; Franklin, E.C.
Biochemistry 19, 4304-4308, 1980
A;Title: Primary structure of human gamma3 immunoglobulin deleti
A;Reference number: A90442; MUID:81021548
A; Molecule type: mRNA
A; Residues: 12-70;72-114;116-125,'E',127-133,'L',135-136,'E',138,'Y',140-154,'D',156-157
A; Note: a carboxyl-terminal Lys is removed posttranslationally
A; Note: this sequence may represent an allelic form or another gamma chain subclass
C; Comment: The heavy chain disease protein Wis is shown.
                                                                                                                                                          A;Molecule type: protein
A;Residues: 59-125, 'EB',128-226,228-289 <WOL>
B; Franklin, E.C.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A;Title: gamma heavy chain disease in man: cDNA sequence supports partial gene deletion A;Reference number: A93915; MUID:82247835
A;Contents: heavy chain disease protein Omm
                                                                                                                                                                                                                                                                                                                                                                              idue segment (12-28)
A;Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, R;Nolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, 1 Biochem. Biophys. Res. Commun. 71, 907-914, 1976
A;Title: The amino acid sequence of "heavy chain disease" prote A;Reference number: A90198; MUID:77021516
A;Contents: heavy chain disease protein Zuc, partial sequence A;Accession: A90198
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                                                                                                                      A;Accession: A93915
A;Moleon's T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Primary structure of the 'hinge' region of human A;Reference number: A92219; MUID:77118561
A;Contents: normal gamma-3 chains, sequence corresponding A;Accession: A92219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchains, Note: this protein lacks most of the V region and all of the CH1 region. Residue 12 ch; Note: the sequence of residues 42-76 was taken from the reference that follows R; Michaelsen, T.E.; Frangione, B.; Franklin, E.C.
J. Biol. Chem. 252, 883-889, 1977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein A; Residues: 1-289 <FRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Reference number: A90442; MUII
A;Contents: heavy chain disease
A;Accession: A90442
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te: the hinge region in gamma-3 chains is about four times
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Pred. No. 2.2e-65;
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A;Molecule type: mRNA A;Roslecule type: mRNA A;Roslecule type: mRNA A;Roslecule type: mRNA A;Roslecule type: m8-103;M/105-143,'E',145-184,'A',186,'E',188-266 <MAR> A;Roslecule 88-103;M/105-143;'E',1103-15111; PIDN:AAA31289.1; PID:916 A;Note: this sequence has the dll allotypic marker, 104-Met, and the R;Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R. Blochem. J. 116, 249-259, 1970 A;Title: Sequence studies of the Fd section of the heavy chain of ral A;Reference number: A90245; MUID:70110015 A;Accession: A90245
A; Molecule type: protein

A; Residues: 132-143, 'E', 145-161 <FRU>

R; Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.

in Gamma Globulins, Nobel Symp. 3, Killander,

A; Reference number: A94416
                                                                                                                                                                                                                                                                                                                            R; Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982 A; Title: Heavy chain genes of rabbit IgG; isolation A; Reference number: A93928; MUID:83299917 A; Accession: A93928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Note: this sequence has the d12 allotypi R;Pratt, D.M.; Mole, L.E. Biochem. J. 151, 337-349, 1975
A;Title: Sequence studies on the constant A;Reference number: A90290; MUID:76135469
A;Accession: A90290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Nucleotide sequence of a rabbit IgG A;Reference number: A91749; MUID:84030930 A;Accession: A91749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig gamma chain C region - rabbit C;Species: Oryctcolagus cuniculus (domestic rabbit) C;Species: Oryctcolagus cuniculus (domestic rabbit) C;Date: 24-Apr.1984 *sequence_revision 15-Nov-1984 *text_change C;Accession: A917.49; A90299; A93928; A90245; A94416; A02161 R;Bernstein, K.E.; Alexander, C.B.; Mage, R.G. Immunogenetics 18, 387-397, 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein
A; Residues: 1-47, 'E', 49-71, 'PV', 72-128 <PRA>
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A; Residues: 1-323 <BER>
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A; Map position: 14q32.33-14q32.33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVD 123
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Pred. No. 1.5e
.3; Mismatches
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                      R.E.; Delaney, R.
er, J., ed., pp.109-127,
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1.5e-64;
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J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified A;Reference number: I47158; MUID:95015845
A;Status.
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A; Molecule type: protein
A; Mesidues: 139-131;155-172, 'D',174-184, 'A',186,'E',188-200,'D',202-217,'E',219-232,'Q',
A; Nete: this has the e15 allotypic marker, 185-Ala
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F; 20-82/Domain: immunoglobulin homology <IM2>
F; 213-319/Domain: immunoglobulin homology <IM3>
F; 173/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig gamma 2b chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 *sequence_revision 21-Feb-1997 *text_change 21-Jan-2000
C;Accession: I47160
R;Kacskovics, I.; Sun, J.; Butler, J.E.
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C;Superfamily: immunoglobulin C region; immunoglobulin
F;133-202/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                            Query Match 40.4%; Score 906.5; DB 2; Best Local Similarity 73.2%; Pred. No. 7.5e-51; Matches 164; Conservative 29; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local :
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sidues: 1-328 <KAC>
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                             185
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                                                                                                                                             TISKARGQPLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT:175
FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                  PQVYTLPPHAEELSRSKVSITCLVIGFYPPDIDVEWQRNGQPEPEGNYRTTPPQQDVDGT
                                                                                                  PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--FENNYKTTPPVLDSDGS 184.
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Pred. No. 1.3e-51;
9; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                  Length 328;
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RESULT 13

147159

1497159

179 gamma 2a chain constant region - pig (fragment)
C; Species: Sus scrofa domestica (domestic pig)
C; Species: Sus scrofa domestica (domestic pig)
C; Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C; Date: 21-Feb-1997 #text_change 21-Jan-2000
C; Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #
                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:U03782; NID:g433129; PIDN:AAA52220.1; C;Genetics:
A;Gene: IgG4
C;Superfamily: immunoglobulin C region; immunoglobulin homolog; F;82-151/Domain: immunoglobulin homology <IMY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: 147162
R;Racskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG
A;Reference number: 147158; MUID:95015845
A;Accession: 147162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNA
A;Residues: 1-277 <KAC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig gamma 4 chain constant region - pig (fic) Species: Sus scrofa domestica (domestic C;Date: 21-Feb-1997 #sequence_revision 21-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δÃ
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             285 YFLYSKFSVDKASWQGGGIFQCAVMHEALHNHYTQKSISKTPGK 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            165 TAQTRPKEEQFNSTYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAKGQTRE
   43
                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                               نبر
PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGS
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                                                                                                                               Conservative
                                                                                                                                                          40.2%; Score 903.5; DB 2; 71.1%; Pred. No. 9.6e-51;
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73.2%; Pred. No. 7.5e-51;
                                                                                                                                                                                                                                                                                          region; immunoglobulin homology
homology <IMM>
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21-Feb-1997
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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 227-311 (TR2>
R;Oliveira, B.; Lamm, M.E.
Biochemistry 10, 26-31, 1971
A; Reference number: A90354; MUID:71058474
A; Contents: annotation; disulfide bonds
A; Note: Cys-16 is involved in a heavy-light chain bond
A; Note: Cys-16; Cys-107, and Cys-110 form inter-heavy chain bonds
A; Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds
C; Comment: This chain was isolated from pooled serum of strain 13 inbred guinea p
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical lig
Dain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate
C; Superfamily: immunoglobulin c region; immunoglobulin homology
C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
E; 21-81/Domain: immunoglobulin homology (XIA)
E: 135-204 (Nomain: immunoglobulin homology (XIA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 69-133;312-329 <TUR>
A;Residues: 69-133;312-329 <TUR>
B;Fracey, D.E.; Cebra, J.J.
Biochemistry 13, 4796-4803, 1974
A;Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.
A;Reference number: A90384; MUID:75036072
A;Accession: A90384
F:142-202/Disulfide bonds: #status experimental F:178/Binding site: carbohydrate (Asn) (covalen: F:248-308/Disulfide bonds: #status experimental
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A;Residues: 4-68 <BIR>
A;Residues: K.J.; Cebra, J.J.
Biochemistry 10, 9-17, 1971
Biochemi
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A;Residues: 1-3 <TRI>
A;Residues: 1-3 <TRI>
R;Birshtein, B.K.; Hussain, Q.Z.; Cebra, J.J.
Biochemistry 10, 18-25, 1971
A;Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III.
A;Reference number: A90352; MUID:71058471
A;Accession: A90352
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                                                                                                                                                                   F;135-204/Domain: immunoglobulin homology <IM2>F;241-310/Domain: immunoglobulin homology <IM3>F;28-79/Disulfide bonds: #status experimental
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A;Residues: 134-226 <TRA>
R;Residues: 134-26 <TRA>
R;Trischmann, T.M.; Cebra, J.J.
Chemistry 13, 4804-4811, 1974
Itle: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.
A;Accession: A90385; MUID:75036073
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;Species: Cavia porcellus (guinea pig);Date: 07-May-1981 #text_change 16-Jul-1999;Date: 07-May-1981 #sequence_revision 07-May-1981 #text_change 16-Jul-1999;Accession: A94553; A90352; A90359; A90384; A90385; A02151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reference number: A94553
Accession: A94553
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mitted to the Atlas, April 1975
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                                                            (covalent) #status experimental
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                               184 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 227
                                                                                                                                        166 GNAETKPRVEQYNTTFRVESVLPIQHQDWLRGKEFKCKVYNKALPAPIEKTISKTKGAPR 225
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                                                                                                                                                           66 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 125
                                                                                                                                                                                                                                  6 TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 65
MPDVYTLPPSRDELSKSKVSVTCLIINFFPADIHVEWASNRVPVSEKEYKNTPPIEDADG
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Pred. No. 9.7e-50;
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Search completed: December 27, 2000, 10:54:40 Job time: 191 sec

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Maximum Match 100%
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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4: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*
164575 segs, 16761186 residues
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Gapop 10.0 ,
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US-08-284-391B-33

US-08-957-063-16

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US-08-595-043A-50
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US-08-470-299-4
US-08-784-512-3
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PCT-US95-03866-14
PCT-US95-10043-9
PCT-US96-11043-9
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50, Appl
7, Appl
7, Appl
4, Appl
11, Appl
12, Appl
13, Appl
14, Appl
16, Appl
18, Appl
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452 3 US-09-027-449-71 Sequence 71 453 3 US-08-466-151-8 Sequence 8, 454 2 US-08-437-642B-22 Sequence 22 454 3 US-08-437-642B-22 Sequence 22 454 4 PCT-US93-07832-22 Sequence 20 911 2 US-08-461-968A-5 Sequence 5, 442 1 US-08-462-571-5 Sequence 5, 446 2 US-08-462-571-5 Sequence 1, 486 1 US-08-243-010-6 Sequence 1, 488 1 US-08-243-010-6 Sequence 1, 488 1 US-08-097-827-11 Sequence 1, 438 1 US-08-97-827-11 Sequence 1, 438 1 US-08-97-827-1 Sequence 1, 438 1 US-08-97-827-1 Sequence 4, 232 1 US-08-590-043-4 Sequence 4, 232 1 US-08-580-014-4 Sequence 4,	1212	1212	1212	1212	1212	1215	1215	1216.5	1216.5	1221	1221	1224	1227	1227	1227	1227	1227
3 US-09-027-449-71 3 US-08-466-151-8 2 US-07-934-373C-22 3 US-08-486-252 3 US-08-487-642B-22 4 PCT-US93-07832-22 5 Sequence 22 2 US-08-484-438-10 1 US-08-461-968A-5 2 US-08-462-571-5 2 US-08-462-571-5 3 US-08-243-010-6 1 US-08-243-010-6 5 Sequence 11 1 US-08-243-07832-21 1 US-08-243-07832-21 1 US-08-243-078-27-11 1 US-08-243-078-27-11 1 US-08-243-078-27-11 1 US-08-259-08-34 1 US-08-580-078-28-4 1 US-08-580-078-4 1 US-08-580-078-4 2 Sequence 4, 4 PCT-US95-06530-4 5 Sequence 4,	54.0	54.0	54.0	54.0	54.0	54.1	54.1	54.2	54.2	54.4	54.4	54.5	54.6	54.6	54.6	54.6	54.6
US-09-027-449-71 US-08-466-151-8 US-08-466-151-8 US-07-34-373C-22 US-08-437-642B-22 US-08-437-642B-22 US-08-481-968A-5 US-08-461-968A-5 US-08-462-571-5 US-08-462-571-5 US-08-473-010-1 US-08-243-010-6 US-08-243-010-6 US-08-243-010-6 US-08-243-010-6 US-08-243-011-6 US-08-243-011-6 US-08-243-011-6 US-08-23-11 US-08-23-11 US-08-23-4 US-08-570-23-4 US-08-570-23-4 US-08-590-014-4 US-08-590-014	232	232	232	232	232	438	438	552	486	442	442	911	454	454	454	453	452
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ALIGNMENTS

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RESULT 1
US-07-940-861-43
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/940,861
FILING DATE: 21-CCT-1992
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/US92/02050
FILING DATE: 12-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/667,971
FILING DATE: 12-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/770,967
FILING DATE: 07-CCT-1991
PRIOR APPLICATION NUMBER: US 07/770,967
FILING DATE: 17-CAMPATION.
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                                                                                                                     ATTORNEY AGENT INFORMATION:

NAME: HALEY, James F., Jr.

REGISTRATION UNMBER: 27,794

REFERENCE/DOCKET NUMBER: 3151

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)715-0670

TELEFAX: (212)715-0673

TELEX: 14.8367
                                                                                                  TELEX: 14-8367
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
                                     SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: "OSA, Margaret D.
TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE
TITLE OF INVENTION: FUNCTION ASSOCIATED ANTIGEN 3
NUMBER OF SEQUENCES: 43
  TOPOLOGY: 1:
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CITY: New York
STATE: New York
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ZIP: 100
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10022-6250
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875 Third Avenue
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MILLER, Glenn T.
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protein
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Best Local Similarity
Matches 227; Conserv
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                                                                                                                                                                                          APPLICATION NUMBER: US 07/667,971
FILING DATE: 12-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/770,967
FILING DATE: 07-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: HALEY, James F., Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                      NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,512
FILING DATE: 02-UN-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 12-MAR-1992
                                                                                                                                        REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B151CIP2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                 SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOC:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 VDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKENWYV 179
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TYPE: ami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: New York
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                                                                                                          TELEFAX:
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                                                                                         14-8367
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                             347 amino acids
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                                                                                                        (212)715-0600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ROSA, Margaret D.
VENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE
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Best Local Similarity
Matches 227; Conserv
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GENERAL INFORMATION:
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                                                        TELEFAX: 14-8367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A. ZIP: 10022-6250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
STATE: New York
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02050
FILING DATE: 12-MAR-1992
APPLICATION NUMBER: US 07/667,971
FILING DATE: 12-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/770,967
FILING DATE: 07-0CT-1991
                                                             INFORMATION FOR SEQ ID NO:
                                                                                                 REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)715-0600
TELEFAX: (212)715-0673
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,657
                SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acid
                                                                                                                                                                             FILING DATE: 07-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: HALEY, James F., JI
REGISTRATION NUMBER: 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 VDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 179
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                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 02-JUN-1995
CLASSIFICATION: 424
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875 Third Avenue
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MILLER, Glenn
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amino acids
acid
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Pred. No. 1.2e-97;
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-459-657-43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 54.9
Best Local Similarity 99.0
Matches 227; Conservative
                                       APPLICATION NUMBER: US 07/770,967
FILING DATE: 07-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: HALEY, James F., Jr.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B151CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)715-0600
                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/940,861
FILING DATE: 21-OCT-1992
APPLICATION NUMBER: PCT/US92/02050
FILING DATE: 12-MAR-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/667,971 FILING DATE: 12-MAR-1991 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ROSA, MARGARET D.
TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE
TITLE OF INVENTION: FUNCTION ASSOCIATED ANTIGEN 3
NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: BIOGEN, INC.
APPLICANT: WALLNER, Barbara P.
APPLICANT: MILLER, Glenn T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 875 Thir
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/08460132
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875 Third Avenue
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Pred. No. 1.
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1.2e-97;
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Best Local Sin
Matches 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 43, Application PC/TUS9202050 GENERAL INFORMATION:
                                                                                                     FILING DATE: 12-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/770,967
FILING DATE: 07-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: HALEY, James F., Jr.
REGISTRATION UMBER: 27,794
REFERENCE/DOCKET NUMBER: B151CIP2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, '
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/0205(
FILING DATE: 19920312
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10022-6250
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/667,971
FILING DATE: 12-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: WALLNER, Barbare
APPLICANT: MILLER, Glenn T.
APPLICANT: ROSA, Margaret E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS LENGTH: 347 amino aci TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCRRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ROSA, MARGARET D.
TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE
TITLE OF INVENTION: FUNCTION ASSOCIATED ANTIGEN 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 KGQPREPQVYTLPFSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New York
                                                                TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barbara P.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                     PCT/US92/02050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1234; DB 2;
Pred. No. 1.2e-97;
1; Mismatches 0;
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TOPOLOGY: linear protein

ENGTH:

AMINO ACID

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                                  Matches
                                                     Query Match
Best Local
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                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                               REGISTRATION NUMBER: 32,837
REFERENCE,DOCKET NUMBER: SG.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPAX: (415) 397-8338
                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 31-JAN-19
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION: NAME: CARROLL, PETER G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                  Local 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 VDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240
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                                                                                                                                                                         LENGTH: 232 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: ZZU ......
STATE: SAN FRANCISCO
STATE: CALIFORNIA
TWITTED STA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 99.0 nes 227; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION:
                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         220 MONTGOMERY STREET, SUITE 2200
                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGARLATO, GREGORY D
                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIEN & CARROLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                           protein
                                                                                                                                                                                                                                                                                                                                                                                          31-JAN-1996
                                                                                                                                                                                                                                                                                                           JFONEL., PETER G. 32,837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54.9%;
99.6%;
                                                     54.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN EXPRESSION SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                             US/08/595,043A
                                 Score 1233; DB 2;
; Pred. No. 8.3e-98;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1234; DB 4;
Pred. No. 1.2e-97;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                        SGAR-00371
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                                                                  Length 232;
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                                    Indels
                                  0;
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Best Query Match

Local

1 Similarity 100 227; Conservative

100.0%;

0;

Mismatches

54.9%; Score 1233; DB 1; 100.0%; Pred. No. 1.6e-97;

Length 371; Indels

0;

Gaps

0

Matches

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US-08-236-311-7
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                                                                                      INFORMATION FOR SEQ ID NO:
                                            SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acid
                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/104329
FILING DATE: 02-0CT-1987
                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/250785
FILING DATE: 28-SEP-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
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MEDIUM TYPE: 5.25 in
                                                                                                                                      TELEPHONE: 415/225-1896
                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 26-AUG-PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
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                                                                                        TELEFAX: 417/77168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: South San Francisco
STATE: California
                                                                                                                                                                          REGISTRATION NUMBER: 28
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                                                                         415/952-9881
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26-AUG-1992
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18-FEB-1992
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                                                                                                                                                                                                           Janet E.
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                                        TOPOLOGY: US-08-457-918-7
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FILING DATE: 18-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/250785
FILING DATE: 28-SEP-1988
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATE: 07/104329
FILING DATE: 02-OCT-1987
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                                                                       TELEX: 910/371-7168
(INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 07/936190
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/842777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/236311
EFILING DATE: 02-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8228
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
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APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION: Adheson Variants
                                                                                                                                                                                                                                                                                          FILING DATE: 02-OCT-1987
ATTORNEY/AGENT INFORMATION:
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CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/
FILING DATE: 1-JUN-1995
                                                                                                                                                                                                                                                     NAME: Kubinec, Jeffrey S. REGISTRATION NUMBER: 36,5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
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ER: P0444P1C3
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                                                                     Query Match
Best Local Similarity
Matches 227; Conserv
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Conservative

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Mismatches

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Indels

Gaps

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; TYPE: , amino acid
; STRANDEDNETS:
; TOPOLOGY: linear
US-08-470-299-4
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                                                                                                                                                                                   TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/
FILING DATE: 06-7UN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SUTTON, Jeffrey A.
REGISTRATION NUMBER: 34,02
REFERENCE/DOCKET NUMBER: 9
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 387 amino acids
                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Shatzman, Allan R.
TITLE OF INVENTION: No. 5783181el Compounds
NUMBER OF SEQUENCES: 21
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T: 709 Swedeland
King of Prussia
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Young, Peter R.
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Kay E.
54.9%;
100.0%;
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Score 1233; DB 1; pred. No. 1.7e-97;
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                  Length 387;
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US-08-784-512-3
                                                                  Query Match 54.9%; Score 1233; DB 2; Best Local Similarity 100.0%; Pred. No. 1.7e-97; Matches 227; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                               TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 187/
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                              MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: EP 9610
FILING DATE: 18-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: GRANDOS, PATICIA D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/0 FILING DATE: 17-JAN-1997 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: and native aggrecan to study the proteolytic
TITLE OF INVENTION: "Aggrecanase" in cell culture systems
     170
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                                                                                                                                                                        NAME/KEY:
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                               LENGTH:
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GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
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                                                                                                                                                                                                                                                                                               396 amino acids
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Suite 500, 3000 K Street, N.W.
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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PCT-US95-03866-12
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Best Local Similarity
Matches 227; Conserv
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SEQUENCE CHARACTERISTICS:
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NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/220
APPLICATION NUMBER: US 08/220
FILING DATE: 28-MAR-19944;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Fish & Neave
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APPLICANT: LOBELL, Robert B (US only)
TITLE OF INVENTION: STABILIZED DIMER OF
TITLE OF INVENTION: FLT-3/FLK-2 LIGAND
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122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
                                                                                                                                     198 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 257
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                                                       258 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 317
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                                                                             62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
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                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                 Score 1233; DB 4;
Pred. No. 1.9e-97;
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Best Local Similarity 100.
Matches 227; Conservative
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NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Cyto
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
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TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: 1 MOLECULE TYPE:
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APPLICATION NUMBER: US 0
FILING DATE: 28-MAR-1994
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APPLICATION NUMBER: PCT/US95/03866
FILING DATE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC PODS,MS-DOS
SOFTWARE: Patentin Release #1.0
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APPLICANT: Lobell, Robert B (US only)
TITLE OF INVENTION: STABLILIZED DIMER OF KIT LIGAND AND
TITLE OF INVENTION: FLT-3/FLK-2 LIGAND
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS;
ADDRESSEE: Fish & Neave
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CITY: New York
STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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                                                                                                    GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
                                                                                                                                                                               GVEVHNAKTKPREEGYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
      DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 424
                                          DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
                                                                                 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 377
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PCT-US96-10043-9
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Sequence 9, Application PC/TUS9610043 GENEFAL INFORMATION:
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; TOPOLOGY: 1:
; MOLECULE TYPE:
PCT-US96-10043-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 00'
REFERENCE/DOCKET NUMBER: 00'
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPAX: 617/542-8906
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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ZIP: 02210-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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PRIOR APPLICATION DATA:
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391
                  182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
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TELEFAX: 200154
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                                                                                                                                                    271 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 330
                                                                                                                                                                                          62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 6 FILING DATE: 14-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                  2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                            GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
                                                                                                                                                                        GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                          GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
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                                                                                                                                                                                                                                                                                                      54.9%; Score 1233; DB 4; ilarity 100.0%; Pred. No. 2e-97; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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?5 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Karen F.
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                                                                                                                                                                                                                                                                                                                                          DB_4; Length 437;
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APPLICANT: The General Hospital Corporation TITLE OF INVENTION: P-SELECTIN LIGANDS AND

RELATED MOLECULES

TITLE OF INVENTION: AN NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:

AND METHODS

ADDATESTREET: 2. STREET: 2. Boston

225 Franklin Street

Fish & Richardson P.C.

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                                                                                                                                           Sequence 13, Application US/08458516 Patent No. 5777085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 54.9%; Sometime 100.0%; I Best Local Similarity 100.0%; I Matches 227; Conservative 0;
                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                             APPLICANT: CO, Man Sung
APPLICANT: TSO, J. Yun
TITLE OF INVENTION: Humanized A
TITLE OF INVENTION: GPIIB/IIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 442 amino acids
TYPE: amino acid
STRANDEDNESS: not releva
TOPOLOGY: linear
MOLECULE TYPE: protein
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FROM PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 00
REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-8906
TELEFAX: 617/542-8906
                 NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Lech, Karen F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 14-JUN-
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
                                                                                                                                                                                                                                                                                                                              336 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
                                                                                                                                                                                                                                                                                                                                                              122 GOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDS 181
                                                                                                                                                                                                                                                         396 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 442
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TELEFAX: 200154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
ADDRESSEE:
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                   ADDRESS
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                                                                    Humanized Antibodies Reactive with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1233; DB 4; 1; Pred. No. 2e-97; 0: Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS LENGTH: 449 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/059,159
FILING DATE: 03-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
                                                                                                                                                                                    343 GQPREPQYYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
                                                                                                                                                                                                                                                                                                                                                      283 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 342
                                                                                                                                                                                                                                                                                                                                                                                                   62 GVEYHNAKTKPREEQYNSTYRVV3VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear
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STATE: California
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100.0%; Pred. No. 2e-97;
Live 0; Mismatches
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Search completed: December 27, 2000, 10:53:58 Job time: 149 sec

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seg length: 2000000000
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   1. _Geneseq_36:*
1. _/SIDS1/gcgdatta/geneseq/geneseqp/AA1980.DAT:*
2. _/SIDS1/gcgdatta/geneseq/geneseqp/AA1981.DAT:*
3. _/SIDS1/gcgdatta/geneseq/geneseqp/AA1982.DAT:*
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Gapop 10.0 , Gapext 0.5
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2246
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342.450 Million cell updates/sec
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                                   Amino acid sequenc
Chimeric receptor
Chimeric receptor
CD2 binding LFA-3-
Human transmembran
Rabbit TGFbetaRII:
Human TGFbetaRII:
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Recombinant human
Recombinant human
 acid
acid
sequenc
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RESULT W48650

Heavy chain of hmAb425 fused to TNF alpha

04-AUG-1998 (first entry)

W48650;

W48650 standard; Protein; 652 AA

ALIGNMENTS

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Region
Bruemmer W, Burge C, Dunker
Rieke E, Von Hoegen I, Welge
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Homo sapiens.
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16-SEP-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antibody-cytokine fusion protein; tricistronic vector; chimeric; TNF alpha; IL-2; IRES; internal ribosome entry site.
                                                                                                                                                                                                                                                                                                                                                        02-SEP-1997;
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                                                                                                                                  (MERE ) MERCK PATENT GMBH.
                                                                                                                                                                                                                           96EP-0115635.
96EP-0114820.
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495..652
/note= "TNF alpha"
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligo:cistronic expression vector - useful for production of, e.g. MAb425/TNF-^a or MAb425/IL-2 antibody fusion protein
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N-PSDB; V18096.
              Recombinant; metFc-OB protein; Fc region; immunoglobulin; Ig; OB; obesity; human; adiposity; blood lipid; diabetes type II; insulin; hypoglycaemic; anthypertensive; diuretic; appetite suppressant; suspension; variant.
                                                                                        Recombinant human metFc-OB
                                                                                                                      05-FEB-1999
                                                                                                                                                    W83963;
                                                                                                                                                                                  W83963 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                             TSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCK-ELQYV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKETFPPKYLHYDEE 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
                                                                                                                                                                                                                                                                                                                   nrranallangvelrdnqlvvpseglyliysqvlfkgqgc-psthvllthtisriavsyq
                                                                                                                                                                                                                                                                                                                                              KQECNR-----THNRVCECKEGRYL-EIEFCLKHRSCPPGFGVVQAGTPERNTVCKR 351
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                                                                                                                                                                                  374
                                                                                      protein variant.
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19; Mismatches
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hes 54; Indels
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W49075;

18-NOV-1998

(first entry)

Recombinant human MetFc-OB variant 2 protein

W49075 standard;

Protein;

374

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RESULT
W49075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This represents a recombinant metFc-OB protein variant which consists of an Fc region of human immunoglobulin [19] fused to a human OB (obesity) protein. The invention provides a human OB protein suspension that: contains at least 0.5 mg/ml of the human OB protein derivatised by attachment of the Fc region of an 19 to the N-terminus of OB, and has a OB H 6-8. The suspensions are used to reduce weight, adiposity and blood lipid levels, to treat or prevent diabetes type II, and to increase lean mass and insulin sensitivity. They may be used in conjunction with insulin, hypoglycaemics, anthypertensives, diuretics, appetite suppressants etc. These suspensions are stable and active at physiological pH and are ready-for-use formulations that do not require physiological pH and are ready-for-use formulations that do not require freezeing or freeze drying. As they are very concentrated, only small volumes are required and they provide a sustained-release effect, with increased potency and reduced frequency of injection.
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Best Local
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reduction of weight and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Concentrated suspension of fusion of obesity protein with Fc immunoglobulin fragment - stable at physiological pH, used for e.g. reduction of weight and blood lipid levels, and for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-594525/50
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17-APR-1997;
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wes 228; Conserv
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                                                                                                                                                            MDKTHTCPPCPAPELLGGPSVELFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
                                                                                                                                                                                                                        kgqprepqvytlppsrdeltknqvsltclvkgfypsdiavewesngqpennykttppvld
                                                                                                                                                                                                                                                                                                                                           mdkthtcppcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnwyv
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97US-0843971.
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                                                                                                                                                                                                                                                                                                                                                                                                                    55.1%;
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Matches 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant human MetFc-OB variant 2 protein; chimeric; immunoglobulin; high blood lipid level; arterial sclerosis; stroke; Fc-OB fusion protein; diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New fusion proteins of OB and Fc \, used for treating e.g. excess weight, diabetes, arterial sclerosis, arterial plaque, high blood lipid level, gall stones or stroke
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                                                                                                                                                                                     DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
                                                                                                                                                                                                                                                                  MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTIMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1998-377658/32
DB; V32902.
                   SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
                                                                                                      KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
sdgsfflyskltvdksrwqqgnvfscsvmhealhnhytqkslslspgk
                                                                            \verb|kgqprepqvytlppsrdeltknqvsltclvkgfypsdiavewesngqpennykttppvld|
                                                                                                                                                                dgvevhnaktkpreegynstyrvvsvltvlhqdwlngkeykckvsnkalpapiektiska 120
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2..374
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                                                                                                                                                                                                                                                                                                                              Score 1238; DB 19;
Pred. No. 6.1e-76;
0; Mismatches 0;
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Best Local (
                                                                                                                                                                                                                             This can be used for modulating a mammalian immune system wherein, the bloactive substance is an antigen characteristic of a pathogen of an autoimmune disease, an allergen, or a tumour. The delivering method is used to deliver therapeutics, including chemotherapy agents, cytokines including incerferon, hormones, including insulin and human growth hormone, fertility drugs, calcitonon, calcitized and other bloactive steroids to intestinal, mucosal and lung epithelium. The method is also used for transepithelial delivery of antigens to provoke tolerance and immunity. The method provides an immunisation, that specifically targets the mucosal surfaces, and does not have the risks associated with injections, including needle transmission of AIDS or hepatitits, of prior art immunisation methods. The present sequence represents the amino acid sequence of an Fc fragment of human immunoglobulin IgG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to methods of delivering molecules to a mammal by administering a conjugative of a therapeutic or a bioactive substance, and an FoRn binding partner targeted to epithelial cells expressing FCRn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Delivering therapeutics, particularly antigens to epithelial cells -comprises use of a conjugate of the therapeutic and an FcRn binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pathogen; autoimmune disease; allergen; tumour; therapeutic; cytokine;
chemotherapy agent; interferon; insulin; human growth hormone; fertility;
drug; calcitonon; steroid; immunity; mucosal; AIDS; hepatitis; Fc; human;
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                                                                                                                                                                                                   Sequence
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(UYBR-) UNIV BRANDEIS.
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                    61
                                                                                                                                    Local Similarity
                                                                                    1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
                                                 RS,
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97.4%;
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                                                                                                                                  Score 1237; DB 20; Pred. No. 4.1e-76;
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       from DNA cassettes encoding each receptor component. In a claimed cell activation process an effector cell is transformed with DNA encoding a chimeric receptor containing 2 or more different cytoplasmic signalling components. Also claimed is use of DNA encoding a recombinant chimeric receptor in a DNA delivery system. The DNA delivery systems can be used for the activation of cells to provide e.g. an increase in cell proliferation, expression of cytokines with e.g. pro- or anti-inflammatory responses, stimulation of cytolytic activity, differentiation or other effector functions, antibody secretion, phagocytosis, tumour infiltration and/or increased adhesion. They can be used in the treatment of e.g. infectious disease, inflammatory disease, cancer, allergic/atopic disease, congenital disease, dermatologic disease, neurologic
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                                                                                                                                                                                                                                                         This protein comprises a chimeric receptor consisting of an scFv engineered from anti-CD3 human antibody CTWO1 linked to an extracellular spacer comprising the human IgG1 hinge, CH2 and CH3, linked to transmembrane and intracellular regions of the human T cell receptor zeta chain. It can be expressed in host cells (e.g. Jurkat) using a chimeric receptor gene (see T90512) constructed
                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                   New DNA systems for activating cells - comprising DNA coding chimeric receptor comprising 2 or more different cytoplasmic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        In particular, they can be used in the treatment of rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, asthma, eczema, cystic fibrosis, sickle cell anaemia, psoriasis, multiple sclerosis, organ or tissue transplant rejection, graft-versus-host disease or diabetes (claimed).
                                                                                                                                                         Chimeric - Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                      W26650 standard; Protein; 692
           (CLLT ) CELLTECH THERAPEUTICS LTD
                                          21-DEC-1995;
                                                                                                 03-JUL-1997
                                                                                                                             WO9723613-A2
                                                                                                                                                                                     graft versus host disease; human; therapy
                                                                                                                                                                                                    psoriasis; multiple sclerosis; transplant rejection;
                                                                                                                                                                                                                                                                                                                  Chimeric receptor hCTMO1/G1/zeta-CD28.
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Pred. No. 1.5e-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Sim:
Matches 258;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease or diabetes (claimed).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                              TSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKELQYVK 301
                                                                                                                                                                                                                                                                                                                                                                                           ggprepqvytlppsreemtknqvsltclvkgfypsdlavewesngqpennykttppvlds 467
                                                                                                                                                                                                                                                                                                                                                                                                                                               GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
-knpqegly-nelqkdkmaeayseigmkgerrrgkg---hdglyqglstatk 637
                                                                                                 vkfsrsadapayqqgqnqlyn---elnlgrreeydvldkrrgrdpemg----gkprr---
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                                                                                                                                                  -------QECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1236.5; DB 18
Pred. No. 1:6e-75;
Pred. No. 1:6e-75;
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Query Match Best Local S Matches 227

Similarity 99.

54.9%; 99.6%;

Score 1234; DB 13; Pred. No. 1e-75; 1; Mismatches 0;

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RESULT
R27163
  The plasmid pSAB152 contains the DNA sequence encoding the LFA-3 signal sequence, the amino terminal 92 amino acids of mature LFA-3, ten amino acids of the hinge region of IgG1 and the CH2 and CH3 constant domains of IgG1 (see Q28678-9 and Q28681-2 for details of the construction of pSAB152). A NotI fragment containing the coding sequence of pSAB152 was used in the construction of expression vector pMDR(92)Ig-3 which can be stably maintained in CHO cells to achieve continuous expression of LFA3TIP. The fusion protein can bind to CD2 and inhibit T cell activation, making it useful to the stable to the content of th
                                                                                                                                                                                                                                                                                                                                                                                    CD2-binding domain of lymphocyte function associated antigen-3 and DNA — for diagnosing and treating inflammation and auto:immune diseases, e.g. systemic lupus erythematosus and rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-MAR-1991;
07-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lymphocyte associated antigen-3; T-lymphocyte accessory molecule; deletion mutant; CD2 binding site; immunomodulator; immunoglobulin; preLFA3TIP; LFA-3(92)IGG; pSAB152; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R27163 standard; Protein; 347 AA
Sequence
                                                                                                                                                                                                                                                                                                                                         Claim 13; Fig 12; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; Q28684.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-MAR-1992;
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                                                  immunomodulation.
  347
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  AA;
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91US-0770967.
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240..347
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29..120
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1..28
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                                                                                                                   Modulation of LFA3/CD2 interaction by administration of a CD2 binding agent inhibits CD2 signalling and T cell proliferation and activation and more particularly modulates the number and/or distribution of memory effector T lymphocytes. The method can be used for treating a condition in a subject where the condition is characterized by memory effector T lymphocytes playing a role in the pathogenesis of the condition such as psoriatic arthritis, rheumatoid arthritis, multiple sclerosis, atopic dermatitis, uveitis, inflammatory bowel disease, Crohn's disease, ulcerative colitis and cutaneous T cell lymphoma and where the method comprises administering to the subject an amount of CD2 binding agent sufficient to modulate the memory effector T lymphocytes. The methods provide inhibition of T cell specific interactions for all antigens present, inhibition of T cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Selective modulation of memory effector T lymphocytes by administration of a CD2 binding agent which inhibits the CD2/LFA-3 interaction useful for treating conditions such as inflammatory bowel diseases, psoriatic arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 75-76; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  memory effector T lymphocyte; psoriatic arthritis;
rheumatoid arthritis; multiple sclerosis; atopic dermatitis;
uveitis; inflammatory bowel disease; Crohn's disease;
ulcerative colitis; cutaneous T cell lymphoma; inhibition; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Y83136 standard;
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                                                                 tolerance
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ector T lymphocyte; psoriatic arthritis;
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                                                                                              immunosuppression,
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                                                                                              t, inhibition of T cell possibly induction of
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Best Local :
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This sequence is a fusion protein of the rabbit transforming growth factor-beta receptor II (TGF-betaRII) and an antibody Fc region. The encoded protein is an example of a protein of the invention, which are isolated TGF-beta receptor fusion proteins that competitively inhibit binding of TGF-beta to TGF-beta receptor. The fusion protein can be used in a method for lowering the levels of TGF-beta in an individual having arthritis. It can also be used to treat medical conditions such as fibroproliferative disorders. The fibroproliferative disorder is a kidney, intraocular or pulmonary fibrosis, especially selected from diabetic nephropathy, or myelofibrosis. The fusion proteins can also be use to treat collagen vascular disorders, including systemic sclerosis, polymyositis, scleroderma, dermatomyositis, and systemic lupus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transforming growth factor-beta receptor; TGF-beta receptor; arthritis; fusion protein; fibroproliferative disorder; diabetic nephropathy; glomerulonephritis; proliferative vitreoretinopathy; myelofibrosis; collagen vascular disorder; therapy; rabbit.
                                                                                                                                                                                                                    Transforming growth factor-beta receptor treat fibroproliferative disorders
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                                                                                                                                                                                            Claim 4; Page 18-19; 70pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9848024-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rabbit TGFbetaRII:Fc protein
                                                                                                                                                                                                                                                                                                                                 (BEOJ ) BIOGEN INC.
                                                                                                                                                                                                                                                                                                                                                            18-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                      16-APR-1998;
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DB; V08998.
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                                                                                                                                                                                                                                                                                                       Koteliansky
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                       Sanicola-Nadel
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RESULT
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Best Local S
Matches 227
                                  This sequence is a fusion protein of the human transforming growth factor-beta receptor II (TGF-betaRII) and an antibody Fc region. The encoded protein is an example of a protein of the invention, which are isolated TGF-beta receptor fusion proteins that competitively inhibit binding of TGF-beta to TGF-beta receptor. The fusion protein can be used in a method for lowering the levels of TGF-beta in an individual having
                                                                                                                                                 Transforming growth factor-beta treat fibroproliferative disorde
                                                                                                                                                                                                                             Cate
                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                   glomerulonephritis; proliferative vitreoretinopathy; myelofibrosis; collagen vascular disorder; therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                             Transforming growth factor-beta receptor; TGF-beta receptor; arthritis; fusion protein; fibroproliferative disorder; diabetic nephropathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human TGFbetaRII:Fc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W73514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         erythematosus. They can also be administered following coronary angioplasty, to prevent restenosis or scarring and reclosing of
          arthritis. It can also be used to treat medical conditions such as fibroproliferative disorders. The fibroproliferative disorder is a
                                                                                                                           Claim 4;
                                                                                                                                                                                                                                                    (BIOJ ) BIOGEN
                                                                                                                                                                                                                                                                             18-APR-1997;
                                                                                                                                                                                                                                                                                                    16-APR-1998;
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DB; V08999.
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                                                                                                                                                                                                                             Gotwals
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                                                                                                                                                                                                                            Koteliansky V,
                                                                                                                                                   disorders
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Pred. No. 1.2e-75;
                                                                                                                                                               receptor
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diabetic nephropathy, glomerulonephritis, proliferative vitreoretinopathy, or myelofibrosis. The fusion proteins can all to treat collagen vascular disorders, including systemic scleros polymyositis, scleroderma, dermatomyositis, and systemic lupus erythematosus. They can also be administered following coronary
                                                                                                                                                                                                                                                                                                                                                                                              Splice variant; rabbit; transforming growth factor-beta; TGF-beta; type II receptor; Fc portion; human IgG1; fusion protein; arthritis; fibroproliferative disease; renal; intra-ocular; pulmonary; fibrosis; diabetic nephropathy; glomerulonephritis; collagen vascular disease; proliferative vitreoretinopathy; myelofibrosis; systemic sclerosis;
New fusion protein of a splice variant of transforming growth factor-beta receptor, for inhibiting the growth factor, e.g. treatment of fibrosis
                                                                                                                                                                                                   16-JUN-1999;
                                                                                                                                                                                                                                                               WO9965948-A1.
                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid sequence of TGF-beta type II receptor variant/IgG1 fusion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y54063 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               angioplasty, to prevent restenosis or scarring and reclosing of arteries
                                                                                                          Koteliansky V,
                                                                                                                                                                      16-JUN-1998;
                                                                                                                                                                                                                                 23-DEC-1999
                                                                                                                                                                                                                                                                                                          Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                      post-radiation
                                                                                                                                                                                                                                                                                                                                                                polymyositis; scleroderma; dermatomyositis; systemic lupus erythematosus; restenosis; wound; connective tissue production; adhesion; scarring;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-MAR-2000
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                                                          2000-106083/09
DB; Z45251, Z45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sdgsfflyskltvdksrwqqgnvfscsvmhealhnhytqkslslspgk 388
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                                                                                                                                      ) BIOGEN
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Pred. No. 1.
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sclerosis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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16-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence for TGF-beta type II receptor variant/IgGl fusion
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                                                                   23-DEC-1999.
                                                                                                                                       WO9965948-A1
                                                                                                                                                                                                                                           Synthetic.
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                                                                                                                                                                                                                                                                                                                                        restenosis; wound; connective tissue production;
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99WO-US13629.
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Pred. No. 1.2e
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                           adhesion;
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                                                                                                                                                                                                                                                                                                                                           scarring;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       growth factor beta (TGF-beta) type II receptor fused to the Fc portion of human IgG1. The fusion protein has higher affinity for TGF-beta than fusion proteins comprising the non-variant form of the receptor. The fusion protein contains soluble TGF-beta receptor constructs that are devoid of a transmembrane region (and are secreted from the cell) but retain the ability to bind TGF-beta. The protein competitively inhibits binding of TGF-beta to cellular receptors and/or forms an inactive complex with TGF-beta. The protein is used to reduce levels of TGF-beta, especially fibroproliferative diseases, e.g. renal, intra-ocular or pulmonary fibrosis; diabetic nephropathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glomerulonephritis; proliferative vitreoretinopathy; myelofibrosis; collagen vascular disease, e.g. systemic sclerosis, polymyositis, scleroderma, dermatomyositis or systemic lupus crythematosus; and fibrosis associated with restenosis. It is also used for treating wounds, to prevent overproduction of connective tissue and so prevent adhesions or scarring, and to prevent post-radiation fibrosis (by administration to patients about to undergo radiation therapy).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New fusion protein of a splice variant of transforming growth factor-beta receptor, for inhibiting the growth factor, e.g. in treatment of fibrosis \,
                                                                                   31-JUL-2000
                                                                                                                Y70867;
                                                                                                                                             Y70867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a splice variant of a human transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Koteliansky V, Gotwals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BIOJ ) BIOGEN INC.
                                                                                                                                                                                                                                                                                                                                      221
                                                                                                                                                                                                                     341
                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                               281
                                                                                                                                                                                                                                                                                                         121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD
                                                                                                                                                                          13
                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                           SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                     sdgsfflyskltvdksrwqqgnvfscsvmhealhnhytqkslslspgk
                                                                                                                                                                                                                                                                              kgqprepqvytlppsrdeltknqvsltclvkgfypsdiavewesngqpennykttppvld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000-106083/09
                                                                                                                                             standard; Protein; 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Z45253, Z45254.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                388
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                   (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0089452.
                                                                                   entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54.9%;
99.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ָם,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1234; DB 21;
Pred. No. 1.2e-75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sanicola-Nadel M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                        388
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Human; interferon-beta-la; IFN-beta-la; immunoglobulin; fusion angiogenesis; antisclerotic; antiinflammatory; immunosuppressiv

flammatory; immunosuppressive; cancer; antiangiogenic; treatment; fibrosis;

protein;

interferon-beta-la/mouse IgG2a Fc fusion protein

Human

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                                                                                                                                                                                                                                                                                   Query Match
Best Local Sim
Matches 227;
                                                                                                                                                                                                                                                                                                        The patent discloses fusion proteins comprising glycosylated interferon-beta (IFN-beta) especially IFN-beta-la, linker groups and non-IFN-beta proteins, especially an immunoglobulin (Ig) protein. The present sequence is a fusion protein that consists of mature human IFN-beta-la and mouse IgG2a Fc domain separated by an enterokinase linker. The fusion protein is useful for inhibiting angiogenesis in a patient. It may also be used to treat multiple sclerosis, fibrosis, inflammatory and autoimmune diseases, cancers, hepatitis and viral infection characterised by
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fusion proteins comprising interferon-beta-la useful for inhibiting angiogenesis \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Whitty A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-1998;
16-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          multiple sclerosis; inflammatory disease; autoimmune disease; hepatitis; viral infection; neovascularisation; mouse; IgG2a Fc domain.
                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                               neovascularisation
                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Fig 2; 82pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BIOJ ) BIOGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200023472-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
  352
                           181
                                                   292
                                                                           121
                                                                                                     232
                                                                                                                                                       172
                                                                                                                                                                                                                   Local Similarity
                                                                                                                              61
                                                                                                                                                                 1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
                                                                                                              DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
                                                                                                                                                     vdkthtcppcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnwyv 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000-339654/29
                                                                                                  dgvevhnaktkpreegynstyrvvsvltvlhqdwlngkeykckvsnkalpapiektiska
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                                                                                                                                                                                                                                                                      399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                      Ą,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0104491
99US-0120237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US24200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= natural_human_IFN-beta-la
167..171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Mouse_IgG2a_Fc_portion
/note= "comprises the hinge region,
constant domains of mouse Ig"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172..399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Enterokinase_linker
                                                                                                                                                                                                                   54.9%;
99.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brickelmaier
                                                                                                                                                                                                       ٠.
                                                                                                                                                                                                     Score 1234; DB 21; Pred. No. 1.2e-75; 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hochman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ָס
                                                                                                                                                                                                                               Length
                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                  399;
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                                                                                                     291
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RESULT

Conservative

Indels

0

Gaps

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Y70868
ID Y70868 standard; Protein; 41
XX
AC Y70868;
XX
AC Y70868;
XX
DT 31-JUL-2000 (first entry)
XX
DE Human interferon-beta-la Glf
XX
KW Human; interferon-beta-la; l
KW angiogenesis; antisclerotic;
KW multiple sclerosis; inflamme
KW viral infection; neovascular
KW vascular cell adhesion molec
OS Homo sapiens.
OS Synthetic.
XX
Key Location/Qua
FT Peptide 1.24
FT /label- vCA
FT /label- "Vasc
FT /label- "Nate
F
Query Match
Best Local Similarity
Matches 227; Conserv
                                                                                                                                                                                                                                 The patent discloses fusion proteins comprising glycosylated interferon beta (IFN-beta) especially IFN-beta-la, linker groups and non-IFN-beta proteins, especially an immunoglobulin (Ig) protein. The present sequence is a fusion protein consisting of a vascular cell adhesion molecule-l (VCAM-l) signal sequence, a modified human IFN-beta-la and human IgGl Fc domain, which are directly fused without a linker sequence. The fusion protein is useful for inhibiting anglogenesis in a patient. It may also be used to treat multiple sclerosis, fibrosis, inflammatory and autoimmune diseases, cancers, hepatitis and viral infection characterised by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label- natural_human_IFN-beta-la
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anglogenesis; antisclerotic; antiinflammatory; immunosuppressive; cancer cytostatic; virucide; hepatotropic; antiinflammatory it reatment; fibrosis; multiple sclerosis; inflammatory disease; autoimmune disease; hepatitis; viral infection; neovascularisation; IgG1 Fc domain; VCAM-1; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fusion proteins comprising interferon-beta-la useful for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; interferon-beta-la; IFN-beta-la; immunoglobulin; fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human interferon-beta-la G162C-IgG1 Fc direct fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                adhesion molecule-1.
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99US-0120237.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= VCAM-1_signal_sequence
/note= "Vascular cell adhesion
25..190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Human_IgGl_Fc_pon
/note= "comprises hinge,
IgGl heavy chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Wild type IFN-beta-la Gly at position 162
substituted by Cys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1..24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Wild
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82pp; English.
                               54.9%;
99.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brickelmaier
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Score 1234; DB 21
Pred. No. 1.3e-75;
1; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ž
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linge, CH2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hochman
                                                           21;
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                                                           Length
                                                              418;
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869 '
Y70869 standard; Protein; 423 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytostatic; virucide; hepatotropic; antiangiogenic; treatment; fibrosis; multiple sclerosis; inflammatory disease; autoimmune disease; hepatitis; viral infection; neovascularisation; IGGI Fc domain; VCAM-1; mutant; vascular cell adhesion molecule-1; G4S linker.
                                                                                                                                                                                                                                                                                                                                                                                                        Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; interferon-beta-la; IFN-beta-la; immunoglobulin; fusion protein; anglogenesis; antisclerotic; antiinflammatory; immunosuppressive; cance
Example 5; Fig 11; 82pp; English
                      Fusion proteins comprising interferon-beta-la useful angiogenesis -
                                                         N-PSDB;
                                                                                         Whitty A, Runkel L,
                                                                                                                                     16-OCT-1998;
16-FEB-1999;
                                                                                                                                                                        15-OCT-1999;
                                                                                                                                                                                               27-APR-2000.
                                                                                                                                                                                                                     WO200023472-A2
                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-JUL-2000 (first entry)
                                                                                                                (BIOJ ) BIOGEN INC.
                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                          Protein
                                                                                                                                                                                                                                                                                                                                                                                          Peptide
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DB; D00168.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interferon-beta-la G162C/G4S linker/IgG1 Fc fusion protein.
                                                                                                                                     98US-0104491.
99US-0120237.
                                                                                                                                                                        99WO-US24200.
                                                                                                                                                                                                                                                                                                                                   /label= natural_human_IFN-beta-la 186
                                                                                                                                                                                                                                                                                                  /note= "Wild type IFN-beta-la Gly at position 162
substituted by Cys"
191..195
                                                                                                                                                                                                                                                                                                                                                         /label= VCAM-1_signal_sequence
/note= "Vascular cell adhesion molecule-1"
25..190
                                                                                                                                                                                                                                         /label= Human_IgG1_Fc_portion
/note= "comprises hinge, CH2 |
IgG1 heavy chain"
                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                       'label= G4S_linker
                                                                                          Brickelmaier M,
                                                                                          Hochman
                                                                                                                                                                                                                                                       CH2 and CH3
                                 for inhibiting
                                                                                                                                                                                                                                                       domains
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Job time: 118 sec
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